



SEQUENCE LISTING

<110> Gurney, et al

<120> ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND USES THEREOF

<130> 28341/6280NCP

<140> US 09/668,314

<141> 2000-09-22

<150> US 60/169,232

<151> 1999-12-06

<150> US 09/416,901

<151> 1999-10-13

<150> US 60/155,493

<151> 1999-09-23

<150> US 09/404,133

<151> 1999-09-23

<150> PCT/US99/20881

<151> 1999-09-23

<150> US 60/101,594

<151> 1998-09-24

<160> 83

<170> PatentIn version 3.1

<210> 1

<211> 1804

<212> DNA

<213> Homo sapiens

<400> 1

atgggagcac tggcccgggc gctgctgctg cctctgctgg ccagtggt cctgcgcgcc 60

gccccggagc tggccccgc gcccttcacg ctgcccctcc gggtgggcgc ggccacgaac 120

cgcgtagttg cgcccccccc gggacccggg acccctgccg agcgccacgc cgacggcttg 180

gcgctcgccc tggagcctgc cctggcgctcc cccgcgggcy cgcgcaactt cttggccatg 240

gtagacaacc tgcaggggga ctctggccgc ggctactacc tggagatgct gatcgggacc 300

ccccgcaga agctacagat tctcgttgac actggaagca gtaactttgc cgtggcagga	360
accccgcaact cctacataga cacgtacttt gacacagaga ggtctagcac ataccgctcc	420
aagggcctttg acgtcacagt gaagtacaca caaggaagct ggacgggctt cgttggggaa	480
gacctcgta ccatcccaa aggcttcaat acttcttttc ttgtcaacat tgccactatt	540
tttgaatcag agaattttctt tttgcctggg attaaatgga atggaatact tggcctagct	600
tatgccacac ttgccaagcc atcaagttct ctggagacct tcttcgactc cctggtgaca	660
caagcaaaca tccccaacgt tttctccatg cagatgtgtg gagccggctt gcccggtgct	720
ggatctggga ccaacggagg tagtcttgtc ttgggtggaa ttgaaccaag tttgtataaa	780
ggagacatct ggtatacccc tattaaggaa gagtgggtact accagataga aattctgaaa	840
ttggaaattg gaggccaaag ccttaatctg gactgcagag agtataacgc agacaaggcc	900
atcgtggaca gtggcaccac gctgctgcgc ctgccccaga aggtgtttga tgcggtggtg	960
gaagctgtgg ccgcgcgcatc tctgattcca gaattctctg atggtttctg gactgggtcc	1020
cagctggcgt gctggacgaa ttcggaaaca ccttgggtctt acttcocctaa aatctccatc	1080
tacctgagag atgagaactc cagcaggtca ttccgtatca caatcctgcc tcagctttac	1140
attcagccca tgatgggggc cggcctgaat tatgaatggt accgattcgg catttcccca	1200
tccacaaatg cgctggtgat cggtgccacg gtgatggagg gcttctacgt catcttcgac	1260
agagcccaga agaggggtggg cttcgcagcg agcccctgtg cagaaattgc aggtgctgca	1320
gtgtctgaaa tttccggggc tttctcaaca gaggatgtag ccagcaactg tgtccccgct	1380
cagtctttga gcgagcccat tttgtggatt gtgtcctatg cgctcatgag cgtctgtgga	1440
gccatcctcc ttgtcttaat cgtcctgctg ctgctgccgt tccgggtgtca gcgtcgcccc	1500
cgtgaccctg aggtcgtcaa tgatgagtcc tctctggtca gacatcgctg gaaatgaata	1560
gccaggcctg acctcaagca accatgaact cagctattaa gaaaatcaca tttccagggc	1620
agcagccggg atcgatggtg gcgctttctc ctgtgccac ccgtcttcaa tctctgttct	1680
gctcccagat gccttctaga ttcaactgtct tttgattctt gattttcaag ctttcaaate	1740
ctccctactt ccaagaaaaa taattaaaaa aaaaacttca ttctaaacca aaaaaaaaaa	1800
aaaa	1804

<210> 2
 <211> 518
 <212> PRT
 <213> Homo sapiens

<400> 2

Met	Gly	Ala	Leu	Ala	Arg	Ala	Leu	Leu	Leu	Pro	Leu	Leu	Ala	Gln	Trp
1			5					10					15		

Leu Leu Arg Ala Ala Pro Glu Leu Ala Pro Ala Pro Phe Thr Leu Pro
 20 25 30

Leu Arg Val Ala Ala Ala Thr Asn Arg Val Val Ala Pro Thr Pro Gly
 35 40 45

Pro Gly Thr Pro Ala Glu Arg His Ala Asp Gly Leu Ala Leu Ala Leu
 50 55 60

Glu Pro Ala Leu Ala Ser Pro Ala Gly Ala Ala Asn Phe Leu Ala Met
 65 70 75 80

Val Asp Asn Leu Gln Gly Asp Ser Gly Arg Gly Tyr Tyr Leu Glu Met
 85 90 95

Leu Ile Gly Thr Pro Pro Gln Lys Leu Gln Ile Leu Val Asp Thr Gly
 100 105 110

Ser Ser Asn Phe Ala Val Ala Gly Thr Pro His Ser Tyr Ile Asp Thr
 115 120 125

Tyr Phe Asp Thr Glu Arg Ser Ser Thr Tyr Arg Ser Lys Gly Phe Asp
 130 135 140

Val Thr Val Lys Tyr Thr Gln Gly Ser Trp Thr Gly Phe Val Gly Glu
 145 150 155 160

Asp Leu Val Thr Ile Pro Lys Gly Phe Asn Thr Ser Phe Leu Val Asn
 165 170 175

Ile Ala Thr Ile Phe Glu Ser Glu Asn Phe Phe Leu Pro Gly Ile Lys
 180 185 190

Trp Asn Gly Ile Leu Gly Leu Ala Tyr Ala Thr Leu Ala Lys Pro Ser
 195 200 205

Ser Ser Leu Glu Thr Phe Phe Asp Ser Leu Val Thr Gln Ala Asn Ile
 210 215 220

Pro Asn Val Phe Ser Met Gln Met Cys Gly Ala Gly Leu Pro Val Ala
 225 230 235 240

Gly Ser Gly Thr Asn Gly Gly Ser Leu Val Leu Gly Gly Ile Glu Pro
 245 250 255

Ser Leu Tyr Lys Gly Asp Ile Trp Tyr Thr Pro Ile Lys Glu Glu Trp
 260 265 270

Tyr Tyr Gln Ile Glu Ile Leu Lys Leu Glu Ile Gly Gly Gln Ser Leu
 275 280 285

Asn Leu Asp Cys Arg Glu Tyr Asn Ala Asp Lys Ala Ile Val Asp Ser
 290 295 300

Gly Thr Thr Leu Leu Arg Leu Pro Gln Lys Val Phe Asp Ala Val Val
 305 310 315 320

Glu Ala Val Ala Arg Ala Ser Leu Ile Pro Glu Phe Ser Asp Gly Phe
 325 330 335

Trp Thr Gly Ser Gln Leu Ala Cys Trp Thr Asn Ser Glu Thr Pro Trp
 340 345 350

Ser Tyr Phe Pro Lys Ile Ser Ile Tyr Leu Arg Asp Glu Asn Ser Ser
 355 360 365

Arg Ser Phe Arg Ile Thr Ile Leu Pro Gln Leu Tyr Ile Gln Pro Met
 370 375 380

Met Gly Ala Gly Leu Asn Tyr Glu Cys Tyr Arg Phe Gly Ile Ser Pro
 385 390 395 400

Ser Thr Asn Ala Leu Val Ile Gly Ala Thr Val Met Glu Gly Phe Tyr
 405 410 415

Val Ile Phe Asp Arg Ala Gln Lys Arg Val Gly Phe Ala Ala Ser Pro
 420 425 430

Cys Ala Glu Ile Ala Gly Ala Ala Val Ser Glu Ile Ser Gly Pro Phe
 435 440 445

Ser Thr Glu Asp Val Ala Ser Asn Cys Val Pro Ala Gln Ser Leu Ser
 450 455 460

Glu Pro Ile Leu Trp Ile Val Ser Tyr Ala Leu Met Ser Val Cys Gly
 465 470 475 480

Ala Ile Leu Leu Val Leu Ile Val Leu Leu Leu Leu Pro Phe Arg Cys
 485 490 495

Gln Arg Arg Pro Arg Asp Pro Glu Val Val Asn Asp Glu Ser Ser Leu
 500 505 510

Val Arg His Arg Trp Lys
 515

<210> 3
 <211> 2070
 <212> DNA
 <213> Homo sapiens

<400> 3
 atggcccaag ccctgccctg gctcctgctg tggatgggcg cgggagtgct gcctgcccac 60
 ggcaccacgc acggcatccg gctgcccctg cgcagcggcc tggggggcgc ccccttgggg 120
 ctgcggctgc cccgggagac cgacgaagag cccgaggagc ccggccggag gggcagcttt 180
 gtggagatgg tggacaacct gaggggcaag tcggggcagg gctactacgt ggagatgacc 240
 gtgggcagcc ccccgagac gctcaacatc ctggtggata caggcagcag taactttgca 300
 gtgggtgctg cccccaccc cttcctgcat cgctactacc agaggcagct gtccagcaca 360
 taccgggacc tccggaaggg tgtgtatgtg ccctacaccc agggcaagtg ggaaggggag 420
 ctgggcaccg acctggtaag catcccccat ggccccaacg tcaactgtgcg tgccaacatt 480
 gctgccatca ctgaatcaga caagttcttc atcaacggct ccaactggga aggcatcctg 540
 gggctggcct atgctgagat tgccaggcct gacgactccc tggagccttt ctttgactct 600
 ctggtaaagc agaccacgt tcccaacctc ttctccctgc agctttgtgg tgctggcttc 660
 cccctcaacc agtctgaagt gctggcctct gtcggaggga gcatgatcat tggaggatc 720
 gaccactcgc tgtacacagg cagtctctgg tatacaccca tccggcggga gtggtattat 780
 gaggtcatca ttgtgcgggt ggagatcaat ggacaggatc tgaaaatgga ctgcaaggag 840
 tacaactatg acaagagcat tgtggacagt ggcaccacca accttcgttt gcccaagaaa 900
 gtgtttgaag ctgcagtcaa atccatcaag gcagcctcct ccacggagaa gttccctgat 960
 ggtttctggc taggagagca gctggtgtgc tggcaagcag gcaccacccc ttggaacatt 1020
 ttcccagtca tctactcta cctaattgggt gaggttacca accagtcctt ccgcatcacc 1080
 atccttccgc agcaatacct gcggccagtg gaagatgtgg ccacgtccca agacgactgt 1140
 tacaagtttg ccatctcaca gtcatccacg ggcactgtta tgggagctgt tatcatggag 1200
 ggcttctacg ttgtctttga tcggggccga aaacgaattg gctttgctgt cagcgcttgc 1260
 catgtgcacg atgagttcag gacggcagcg gtggaaggcc cttttgtcac cttggacatg 1320
 gaagactgtg gctacaacat tccacagaca gatgagtcaa ccctcatgac catagcctat 1380
 gtcatggctg ccatctgcgc cctcttcatg ctgccactct gcctcatggg gtgtcagtgg 1440
 cgctgcctcc gctgcctgcg ccagcagcat gatgactttg ctgatgacat ctccctgctg 1500
 aagtgaggag gcccatgggc agaagataga gattcccttg gaccacacct ccgtggttca 1560
 ctttggtcac aagtaggaga caca'gatggc acctgtggcc agagcacctc aggacctcc 1620
 ccaccacca aatgcctctg ccttgatgga gaaggaaaag gctggcaagg tgggttccag 1680
 ggactgtacc tgtaggaaac agaaaagaga agaaagaagc actctgctgg cggggaatact 1740

cttggtcacc tcaaatttaa gtcgggaaat tctgctgctt gaaacttcag ccctgaacct 1800
 ttgtccacca ttccttttaa ttctccaacc caaagtattc ttcttttctt agtttcagaa 1860
 gtactggcat cacacgcagg ttaccttggc gtgtgtccct gtggtaccct ggcagagaag 1920
 agaccaagct tgtttccctg ctggccaaag tcagtaggag aggatgcaca gtttgctatt 1980
 tgctttagag acagggactg tataaacaag cctaacattg gtgcaaagat tgcctcttga 2040
 attaaaaaaaa aaaaaaaaaa aaaaaaaaaa 2070

<210> 4
 <211> 501
 <212> PRT
 <213> Homo sapiens

<400> 4

Met Ala Gln Ala Leu Pro Trp Leu Leu Leu Trp Met Gly Ala Gly Val
 1 5 10 15

Leu Pro Ala His Gly Thr Gln His Gly Ile Arg Leu Pro Leu Arg Ser
 20 25 30

Gly Leu Gly Gly Ala Pro Leu Gly Leu Arg Leu Pro Arg Glu Thr Asp
 35 40 45

Glu Glu Pro Glu Glu Pro Gly Arg Arg Gly Ser Phe Val Glu Met Val
 50 55 60

Asp Asn Leu Arg Gly Lys Ser Gly Gln Gly Tyr Tyr Val Glu Met Thr
 65 70 75 80

Val Gly Ser Pro Pro Gln Thr Leu Asn Ile Leu Val Asp Thr Gly Ser
 85 90 95

Ser Asn Phe Ala Val Gly Ala Ala Pro His Pro Phe Leu His Arg Tyr
 100 105 110

Tyr Gln Arg Gln Leu Ser Ser Thr Tyr Arg Asp Leu Arg Lys Gly Val
 115 120 125

Tyr Val Pro Tyr Thr Gln Gly Lys Trp Glu Gly Glu Leu Gly Thr Asp
 130 135 140

Leu Val Ser Ile Pro His Gly Pro Asn Val Thr Val Arg Ala Asn Ile
 145 150 155 160

Ala Ala Ile Thr Glu Ser Asp Lys Phe Phe Ile Asn Gly Ser Asn Trp
 165 170 175

Glu Gly Ile Leu Gly Leu Ala Tyr Ala Glu Ile Ala Arg Pro Asp Asp
 180 185 190

Ser Leu Glu Pro Phe Phe Asp Ser Leu Val Lys Gln Thr His Val Pro
 195 200 205

Asn Leu Phe Ser Leu Gln Leu Cys Gly Ala Gly Phe Pro Leu Asn Gln
 210 215 220

Ser Glu Val Leu Ala Ser Val Gly Gly Ser Met Ile Ile Gly Gly Ile
 225 230 235 240

Asp His Ser Leu Tyr Thr Gly Ser Leu Trp Tyr Thr Pro Ile Arg Arg
 245 250 255

Glu Trp Tyr Tyr Glu Val Ile Ile Val Arg Val Glu Ile Asn Gly Gln
 260 265 270

Asp Leu Lys Met Asp Cys Lys Glu Tyr Asn Tyr Asp Lys Ser Ile Val
 275 280 285

Asp Ser Gly Thr Thr Asn Leu Arg Leu Pro Lys Lys Val Phe Glu Ala
 290 295 300

Ala Val Lys Ser Ile Lys Ala Ala Ser Ser Thr Glu Lys Phe Pro Asp
 305 310 315 320

Gly Phe Trp Leu Gly Glu Gln Leu Val Cys Trp Gln Ala Gly Thr Thr
 325 330 335

Pro Trp Asn Ile Phe Pro Val Ile Ser Leu Tyr Leu Met Gly Glu Val
 340 345 350

Thr Asn Gln Ser Phe Arg Ile Thr Ile Leu Pro Gln Gln Tyr Leu Arg
 355 360 365

Pro Val Glu Asp Val Ala Thr Ser Gln Asp Asp Cys Tyr Lys Phe Ala
 370 375 380

Ile Ser Gln Ser Ser Thr Gly Thr Val Met Gly Ala Val Ile Met Glu
 385 390 395 400

Gly Phe Tyr Val Val Phe Asp Arg Ala Arg Lys Arg Ile Gly Phe Ala
 405 410 415

Val Ser Ala Cys His Val His Asp Glu Phe Arg Thr Ala Ala Val Glu
 420 425 430

Gly Pro Phe Val Thr Leu Asp Met Glu Asp Cys Gly Tyr Asn Ile Pro
 435 440 445

Gln Thr Asp Glu Ser Thr Leu Met Thr Ile Ala Tyr Val Met Ala Ala
 450 455 460

Ile Cys Ala Leu Phe Met Leu Pro Leu Cys Leu Met Val Cys Gln Trp
 465 470 475 480

Arg Cys Leu Arg Cys Leu Arg Gln Gln His Asp Asp Phe Ala Asp Asp
 485 490 495

Ile Ser Leu Leu Lys
 500

<210> 5
 <211> 1977
 <212> DNA
 <213> Homo sapiens

<400> 5
 atggcccaag ccctgccctg gctcctgctg tggatgggcg cgggagtgct gcctgcccac 60
 ggcacccagc acggcatccg gctgcccctg cgcagcggcc tggggggcgc cccctgggg 120
 ctgcggctgc cccgggagac cgacgaagag cccgaggagc ccggccggag gggcagcttt 180
 gtggagatgg tggacaacct gaggggcaag tcggggcagg gctactacgt ggagatgacc 240
 gtgggcagcc ccccgagac gctcaacatc ctggtggata caggcagcag taactttgca 300
 gtgggtgctg cccccaccc ctctcctgcat cgctactacc agaggcagct gtccagcaca 360
 taccgggacc tccggaaggg tgtgtatgtg ccctacaccc agggcaagtg ggaaggggag 420
 ctgggcaccg acctggttaag catcccccat ggccccaacg tcaactgtgcg tgccaacatt 480
 gctgccatca ctgaatcaga caagttcttc atcaacggct ccaactggga aggcatacctg 540
 gggctggcct atgctgagat tgccaggctt tgtggtgctg gcttccccct caaccagtct 600
 gaagtgtcgg cctctgtcgg agggagcatg atcattggag gtatcgacca ctgcgtgtac 660
 acaggcagtc tctggtatac acccatccgg cgggagtggt attatgaggt gatcattgtg 720
 cgggtggaga tcaatggaca ggatctgaaa atggactgca aggagtacaa ctatgacaag 780
 agcattgtgg acagtggcac caccaacctt cgtttgccca agaaagtgtt tgaagctgca 840
 gtcaaatcca tcaaggcagc ctctccacg gagaagttcc ctgatggttt ctggctagga 900
 gagcagctgg tgtgctggca agcaggcacc accccttgga acattttccc agtcatctca 960
 ctctacctaa tgggtgaggt taccaaccag tccttccgca tcaccatcct tccgcagcaa 1020
 tacctgcggc cagtggaaga tgtggccacg tccaagacg actgttacia gtttgccatc 1080
 tcacagtcac ccacgggcac tgttatggga gctgttatca tggaggggctt ctacgttgctc 1140

tttgatcggg cccgaaaacg aattggcttt gctgtcagcg cttgccatgt gcacgatgag 1200
 ttcaggacgg cagcgggtgga aggccctttt gtcaccttgg acatggaaga ctgtggctac 1260
 aacattccac agacagatga gtcaaccctc atgaccatag cctatgtcat ggctgccatc 1320
 tgcgccctct tcatgtgcc actctgcctc atggtgtgtc agtggcgctg cctccgctgc 1380
 ctgcgccagc agcatgatga ctttgtgat gacatctccc tgctgaagtg aggaggccca 1440
 tgggcagaag atagagattc ccctggacca cacctccgtg gttcactttg gtcacaagta 1500
 ggagacacag atggcacctg tggccagagc acctcaggac cctccccacc caccaaattgc 1560
 ctctgccttg atggagaagg aaaaggctgg caaggtgggt tccagggact gtacctgtag 1620
 gaaacagaaa agagaagaaa gaagcactct gctggcggga atactcttgg tcacctcaaa 1680
 tttaagtcgg gaaattctgc tgcttgaaac ttcagccctg aacctttgtc caccattcct 1740
 ttaaattctc caacccaaag tattcttctt ttcttagttt cagaagtact ggcattcacac 1800
 gcaggttacc ttggcgtgtg tccctgtggt accctggcag agaagagacc aagcttgttt 1860
 ccctgctggc caaagtcagt aggagaggat gcacagtttg ctatttgctt tagagacagg 1920
 gactgtataa acaagcctaa cattggtgca aagattgcct cttgaaaaaa aaaaaaa 1977

<210> 6
 <211> 476
 <212> PRT
 <213> Homo sapiens

<400> 6

Met Ala Gln Ala Leu Pro Trp Leu Leu Trp Met Gly Ala Gly Val
 1 5 10 15

Leu Pro Ala His Gly Thr Gln His Gly Ile Arg Leu Pro Leu Arg Ser
 20 25 30

Gly Leu Gly Gly Ala Pro Leu Gly Leu Arg Leu Pro Arg Glu Thr Asp
 35 40 45

Glu Glu Pro Glu Glu Pro Gly Arg Arg Gly Ser Phe Val Glu Met Val
 50 55 60

Asp Asn Leu Arg Gly Lys Ser Gly Gln Gly Tyr Tyr Val Glu Met Thr
 65 70 75 80

Val Gly Ser Pro Pro Gln Thr Leu Asn Ile Leu Val Asp Thr Gly Ser
 85 90 95

Ser Asn Phe Ala Val Gly Ala Ala Pro His Pro Phe Leu His Arg Tyr
 100 105 110

Tyr Gln Arg Gln Leu Ser Ser Thr Tyr Arg Asp Leu Arg Lys Gly Val
 115 120 125

Tyr Val Pro Tyr Thr Gln Gly Lys Trp Glu Gly Glu Leu Gly Thr Asp
 130 135 140

Leu Val Ser Ile Pro His Gly Pro Asn Val Thr Val Arg Ala Asn Ile
 145 150 155 160

Ala Ala Ile Thr Glu Ser Asp Lys Phe Phe Ile Asn Gly Ser Asn Trp
 165 170 175

Glu Gly Ile Leu Gly Leu Ala Tyr Ala Glu Ile Ala Arg Leu Cys Gly
 180 185 190

Ala Gly Phe Pro Leu Asn Gln Ser Glu Val Leu Ala Ser Val Gly Gly
 195 200 205

Ser Met Ile Ile Gly Gly Ile Asp His Ser Leu Tyr Thr Gly Ser Leu
 210 215 220

Trp Tyr Thr Pro Ile Arg Arg Glu Trp Tyr Tyr Glu Val Ile Ile Val
 225 230 235 240

Arg Val Glu Ile Asn Gly Gln Asp Leu Lys Met Asp Cys Lys Glu Tyr
 245 250 255

Asn Tyr Asp Lys Ser Ile Val Asp Ser Gly Thr Thr Asn Leu Arg Leu
 260 265 270

Pro Lys Lys Val Phe Glu Ala Ala Val Lys Ser Ile Lys Ala Ala Ser
 275 280 285

Ser Thr Glu Lys Phe Pro Asp Gly Phe Trp Leu Gly Glu Gln Leu Val
 290 295 300

Cys Trp Gln Ala Gly Thr Thr Pro Trp Asn Ile Phe Pro Val Ile Ser
 305 310 315 320

Leu Tyr Leu Met Gly Glu Val Thr Asn Gln Ser Phe Arg Ile Thr Ile
 325 330 335

Leu Pro Gln Gln Tyr Leu Arg Pro Val Glu Asp Val Ala Thr Ser Gln
 340 345 350

Asp Asp Cys Tyr Lys Phe Ala Ile Ser Gln Ser Ser Thr Gly Thr Val
 355 360 365

Met Gly Ala Val Ile Met Glu Gly Phe Tyr Val Val Phe Asp Arg Ala
 370 375 380

Arg Lys Arg Ile Gly Phe Ala Val Ser Ala Cys His Val His Asp Glu
 385 390 395 400

Phe Arg Thr Ala Ala Val Glu Gly Pro Phe Val Thr Leu Asp Met Glu
 405 410 415

Asp Cys Gly Tyr Asn Ile Pro Gln Thr Asp Glu Ser Thr Leu Met Thr
 420 425 430

Ile Ala Tyr Val Met Ala Ala Ile Cys Ala Leu Phe Met Leu Pro Leu
 435 440 445

Cys Leu Met Val Cys Gln Trp Arg Cys Leu Arg Cys Leu Arg Gln Gln
 450 455 460

His Asp Asp Phe Ala Asp Asp Ile Ser Leu Leu Lys
 465 470 475

<210> 7
 <211> 2043
 <212> DNA
 <213> Mus musculus

<400> 7
 atggccccag cgctgcactg gctcctgcta tgggtgggct cggaatgct gcctgcccag 60
 ggaacccatc tcggcatccg gctgcccctt cgcagcggcc tggcagggcc acccctgggc 120
 ctgaggctgc cccgggagac tgacgaggaa tcggaggagc ctggccggag aggcagcttt 180
 gtggagatgg tggacaacct gaggggaaaag tccggccagg gctactatgt ggagatgacc 240
 gtaggcagcc cccacacagac gctcaacatc ctggtggaca cgggcagtag taactttgca 300
 gtgggggctg cccacacccc tttcctgcat cgctactacc agaggcagct gtccagcaca 360
 tatcgagacc tccgaaaggg tgtgtatgtg ccctacaccc agggcaagtg ggagggggaa 420
 ctgggcaccg acctggtgag catccctcat ggccccaacg tcaactgtgc tgccaacatt 480
 gctgcatca ctgaatcgga caagttcttc atcaatggtt ccaactggga gggcatccta 540
 gggctggcct atgtgagat tgccaggccc gacgactctt tggagccctt ctttgactcc 600
 ctggtgaagc agaccacat toccaacatc tttccctgc agctctgtgg cgctggcttc 660
 cccctcaacc agaccgaggc actggcctcg gtgggaggga gcatgatcat tgggtgtatc 720
 gaccactcgc tatacagggc cagtctctgg tacacacca tccggcggga gtggtattat 780
 gaagtgatca ttgtacgtgt ggaaatcaat ggtcaagatc tcaagatgga ctgcaaggag 840
 tacaactacg acaagagcat tgtggacagt gggaccacca accttcgctt gccaagaaa 900

gtatttgaag ctgccgtcaa gtccatcaag gcagcctcct cgacggagaa gttcccggat	960
ggcttttggc taggggagca gctggtgtgc tggcaagcag gcacgacccc ttggaacatt	1020
ttcccagtca tttcacttta cctcatgggt gaagtcacca atcagtcctt ccgcatcacc	1080
atccttcctc agcaatacct acggccgggtg gaggacgtgg ccacgtccca agacgactgt	1140
tacaagttcg ctgtctcaca gtcattccacg ggcactgtta tgggagccgt catcatggaa	1200
ggtttctatg tegtcttcga tcgagcccga aagcgaattg gctttgctgt cagcgcttgc	1260
catgtgcacg atgagttcag gacggcggca gtggaaggtc cgtttgttac ggcagacatg	1320
gaagactgtg gctacaacat tccccagaca gatgagtcaa cacttatgac catagcctat	1380
gtcatggcgg ccatctgcgc cctcttcatg ttgccactct gcctcatggg atgtcagtgg	1440
cgctgcctgc gttgcctgcg ccaccagcac gatgactttg ctgatgacat ctccctgctc	1500
aagtaaggag gctcgtgggc agatgatgga gacgccctg gaccacatct gggtggttcc	1560
ctttggtcac atgagttgga gctatggatg gtacctgtgg ccagagcacc tcaggaccct	1620
caccaacctg ccaatgcttc tggcgtgaca gaacagagaa atcaggcaag ctggattaca	1680
gggcttgac ctgtaggaca caggagaggg aaggaagcag cgttctggtg gcaggaatat	1740
ccttaggcac cacaaacttg agttggaaat tttgctgctt gaagcttcag ccctgaccct	1800
ctgcccagca tcctttagag tctccaacct aaagtattct ttatgtcctt ccagaagtac	1860
tggcgtcata ctcaggctac ccggcatgtg tccctgtggt accctggcag agaaagggcc	1920
aatctcatc cctgctggcc aaagtcagca gaagaagggtg aagtttgcca gttgctttag	1980
tgatagggac tgcagactca agcctacact ggtacaaaga ctgcgtcttg agataaacia	2040
gaa	2043

<210> 8
 <211> 501
 <212> PRT
 <213> Mus musculus

<400> 8

Met	Ala	Pro	Ala	Leu	His	Trp	Leu	Leu	Leu	Trp	Val	Gly	Ser	Gly	Met
1				5				10						15	

Leu	Pro	Ala	Gln	Gly	Thr	His	Leu	Gly	Ile	Arg	Leu	Pro	Leu	Arg	Ser
			20					25					30		

Gly	Leu	Ala	Gly	Pro	Pro	Leu	Gly	Leu	Arg	Leu	Pro	Arg	Glu	Thr	Asp
		35					40					45			

Glu	Glu	Ser	Glu	Glu	Pro	Gly	Arg	Arg	Gly	Ser	Phe	Val	Glu	Met	Val
		50				55					60				

Asp Asn Leu Arg Gly Lys Ser Gly Gln Gly Tyr Tyr Val Glu Met Thr
 65 70 75 80
 Val Gly Ser Pro Pro Gln Thr Leu Asn Ile Leu Val Asp Thr Gly Ser
 85 90 95
 Ser Asn Phe Ala Val Gly Ala Ala Pro His Pro Phe Leu His Arg Tyr
 100 105 110
 Tyr Gln Arg Gln Leu Ser Ser Thr Tyr Arg Asp Leu Arg Lys Gly Val
 115 120 125
 Tyr Val Pro Tyr Thr Gln Gly Lys Trp Glu Gly Glu Leu Gly Thr Asp
 130 135 140
 Leu Val Ser Ile Pro His Gly Pro Asn Val Thr Val Arg Ala Asn Ile
 145 150 155 160
 Ala Ala Ile Thr Glu Ser Asp Lys Phe Phe Ile Asn Gly Ser Asn Trp
 165 170 175
 Glu Gly Ile Leu Gly Leu Ala Tyr Ala Glu Ile Ala Arg Pro Asp Asp
 180 185 190
 Ser Leu Glu Pro Phe Phe Asp Ser Leu Val Lys Gln Thr His Ile Pro
 195 200 205
 Asn Ile Phe Ser Leu Gln Leu Cys Gly Ala Gly Phe Pro Leu Asn Gln
 210 215 220
 Thr Glu Ala Leu Ala Ser Val Gly Gly Ser Met Ile Ile Gly Gly Ile
 225 230 235 240
 Asp His Ser Leu Tyr Thr Gly Ser Leu Trp Tyr Thr Pro Ile Arg Arg
 245 250 255
 Glu Trp Tyr Tyr Glu Val Ile Ile Val Arg Val Glu Ile Asn Gly Gln
 260 265 270
 Asp Leu Lys Met Asp Cys Lys Glu Tyr Asn Tyr Asp Lys Ser Ile Val
 275 280 285
 Asp Ser Gly Thr Thr Asn Leu Arg Leu Pro Lys Lys Val Phe Glu Ala
 290 295 300
 Ala Val Lys Ser Ile Lys Ala Ala Ser Ser Thr Glu Lys Phe Pro Asp
 305 310 315 320

Gly Phe Trp Leu Gly Glu Gln Leu Val Cys Trp Gln Ala Gly Thr Thr
 325 330 335

Pro Trp Asn Ile Phe Pro Val Ile Ser Leu Tyr Leu Met Gly Glu Val
 340 345 350

Thr Asn Gln Ser Phe Arg Ile Thr Ile Leu Pro Gln Gln Tyr Leu Arg
 355 360 365

Pro Val Glu Asp Val Ala Thr Ser Gln Asp Asp Cys Tyr Lys Phe Ala
 370 375 380

Val Ser Gln Ser Ser Thr Gly Thr Val Met Gly Ala Val Ile Met Glu
 385 390 395 400

Gly Phe Tyr Val Val Phe Asp Arg Ala Arg Lys Arg Ile Gly Phe Ala
 405 410 415

Val Ser Ala Cys His Val His Asp Glu Phe Arg Thr Ala Ala Val Glu
 420 425 430

Gly Pro Phe Val Thr Ala Asp Met Glu Asp Cys Gly Tyr Asn Ile Pro
 435 440 445

Gln Thr Asp Glu Ser Thr Leu Met Thr Ile Ala Tyr Val Met Ala Ala
 450 455 460

Ile Cys Ala Leu Phe Met Leu Pro Leu Cys Leu Met Val Cys Gln Trp
 465 470 475 480

Arg Cys Leu Arg Cys Leu Arg His Gln His Asp Asp Phe Ala Asp Asp
 485 490 495

Ile Ser Leu Leu Lys
 500

<210> 9
 <211> 2088
 <212> DNA
 <213> Homo sapiens

<400> 9
 atgctgcccg gtttggcact gtcctgctg gccgcctgga cggctcgggc gctggaggta 60
 cccactgatg gtaatgctgg cctgctggct gaaccccaga ttgccatgtt ctgtggcaga 120
 ctgaacatgc acatgaatgt ccagaatggg aagtgggatt cagatccatc agggaacaaa 180
 acctgcattg ataccaagga aggcacacctg cagtattgcc aagaagtcta ccctgaactg 240
 cagatcacca atgtggtaga agccaaccaa ccagtgacca tccagaactg gtgcaagcgg 300

ggccgcaagc agtgcaagac ccatccccac tttgtgattc cctaccgctg cttagttggt	360
gagtttgtaa gtgatgccct tctcgttcct gacaagtgca aattcttaca ccaggagagg	420
atggatgttt gcgaaactca tcttcactgg cacaccgtcg ccaaagagac atgcagtgag	480
aagagtacca acttgcatga ctacggcatg ttgctgccct gcggaattga caagttccga	540
ggggtagagt ttgtgtgttg cccactggct gaagaaagtg acaatgtgga ttctgctgat	600
gcggaggagg atgactcgga tgtctggtgg ggcgagcag acacagacta tgcagatggg	660
agtgaagaca aagtagtaga agtagcagag gaggaagaag tggctgaggt ggaagaagaa	720
gaagccgatg atgacgagga cgatgaggat ggtgatgagg tagaggaaga ggctgaggaa	780
ccctacgaag aagccacaga gagaaccacc agcattgccca ccaccaccac caccaccaca	840
gagtctgtgg aagaggtggt tcgagttcct acaacagcag ccagtacccc tgatgccgtt	900
gacaagtatc tcgagacacc tggggatgag aatgaacatg cccatttcca gaaagccaaa	960
gagaggcttg aggccaagca ccgagagaga atgtcccagg tcatgagaga atgggaagag	1020
gcagaacgtc aagcaaagaa cttgcctaaa gctgataaga aggcagttat ccagcatttc	1080
caggagaaag tggaatcttt ggaacaggaa gcagccaacg agagacagca gctggtggag	1140
acacacatgg ccagagtgga agccatgctc aatgaccgcc gccgcctggc cctggagaac	1200
tacatcaccg ctctgcaggc tgttcctcct cggcctcgtc acgtgttcaa tatgctaaag	1260
aagtatgtcc gcgcagaaca gaaggacaga cagcacacc taaagcattt cgagcatgtg	1320
cgcatggtgg atcccaagaa agccgctcag atccggtccc aggttatgac acacctccgt	1380
gtgatttatg agcgcatgaa tcagtctctc tcctgtctct acaacgtgcc tgcagtggcc	1440
gaggagattc aggatgaagt tgatgagctg cttcagaaag agcaaaaacta ttcagatgac	1500
gtcttgGCCa acatgattag tgaaccaagg atcagttacg gaaacgatgc tctcatgcca	1560
tctttgaccg aaacgaaaac caccgtggag ctcttccccg tgaatggaga gttcagcctg	1620
gacgatctcc agccgtggca ttcttttggg gctgactctg tgccagccaa cacagaaaac	1680
gaagttgagc ctgttgatgc ccgccctgct gccgaccgag gactgaccac tcgaccaggt	1740
tctgggttga caaatatcaa gacggaggag atctctgaag tgaagatgga tgcagaattc	1800
cgacatgact caggatatga agttcatcat caaaaattgg tgttctttgc agaagatgtg	1860
ggttcaaaca aaggtgcaat cattggactc atggtgggCG gtgttgatcat agcgacagtg	1920
atcgatcatca ccttggtgat gctgaagaag aaacagtaca catccattca tcatggtgtg	1980
gtggaggttg acgccgtgt caccacagag gagcgccacc tgtccaagat gcagcagaac	2040
ggctacgaaa atccaaccta caagttcttt gagcagatgc agaactag	2088

<210> 10
 <211> 695
 <212> PRT
 <213> Homo sapiens

<400> 10

Met Leu Pro Gly Leu Ala Leu Leu Leu Leu Ala Ala Trp Thr Ala Arg
 1 5 10 15

Ala Leu Glu Val Pro Thr Asp Gly Asn Ala Gly Leu Leu Ala Glu Pro
 20 25 30

Gln Ile Ala Met Phe Cys Gly Arg Leu Asn Met His Met Asn Val Gln
 35 40 45

Asn Gly Lys Trp Asp Ser Asp Pro Ser Gly Thr Lys Thr Cys Ile Asp
 50 55 60

Thr Lys Glu Gly Ile Leu Gln Tyr Cys Gln Glu Val Tyr Pro Glu Leu
 65 70 75 80

Gln Ile Thr Asn Val Val Glu Ala Asn Gln Pro Val Thr Ile Gln Asn
 85 90 95

Trp Cys Lys Arg Gly Arg Lys Gln Cys Lys Thr His Pro His Phe Val
 100 105 110

Ile Pro Tyr Arg Cys Leu Val Gly Glu Phe Val Ser Asp Ala Leu Leu
 115 120 125

Val Pro Asp Lys Cys Lys Phe Leu His Gln Glu Arg Met Asp Val Cys
 130 135 140

Glu Thr His Leu His Trp His Thr Val Ala Lys Glu Thr Cys Ser Glu
 145 150 155 160

Lys Ser Thr Asn Leu His Asp Tyr Gly Met Leu Leu Pro Cys Gly Ile
 165 170 175

Asp Lys Phe Arg Gly Val Glu Phe Val Cys Cys Pro Leu Ala Glu Glu
 180 185 190

Ser Asp Asn Val Asp Ser Ala Asp Ala Glu Glu Asp Asp Ser Asp Val
 195 200 205

Trp Trp Gly Gly Ala Asp Thr Asp Tyr Ala Asp Gly Ser Glu Asp Lys
 210 215 220

Val Val Glu Val Ala Glu Glu Glu Glu Val Ala Glu Val Glu Glu Glu
 225 230 235 240

Glu Ala Asp Asp Asp Glu Asp Asp Glu Asp Gly Asp Glu Val Glu Glu
 245 250 255

Glu Ala Glu Glu Pro Tyr Glu Glu Ala Thr Glu Arg Thr Thr Ser Ile
 260 265 270

Ala Thr Thr Thr Thr Thr Thr Thr Glu Ser Val Glu Glu Val Val Arg
 275 280 285

Val Pro Thr Thr Ala Ala Ser Thr Pro Asp Ala Val Asp Lys Tyr Leu
 290 295 300

Glu Thr Pro Gly Asp Glu Asn Glu His Ala His Phe Gln Lys Ala Lys
 305 310 315 320

Glu Arg Leu Glu Ala Lys His Arg Glu Arg Met Ser Gln Val Met Arg
 325 330 335

Glu Trp Glu Glu Ala Glu Arg Gln Ala Lys Asn Leu Pro Lys Ala Asp
 340 345 350

Lys Lys Ala Val Ile Gln His Phe Gln Glu Lys Val Glu Ser Leu Glu
 355 360 365

Gln Glu Ala Ala Asn Glu Arg Gln Gln Leu Val Glu Thr His Met Ala
 370 375 380

Arg Val Glu Ala Met Leu Asn Asp Arg Arg Arg Leu Ala Leu Glu Asn
 385 390 395 400

Tyr Ile Thr Ala Leu Gln Ala Val Pro Pro Arg Pro Arg His Val Phe
 405 410 415

Asn Met Leu Lys Lys Tyr Val Arg Ala Glu Gln Lys Asp Arg Gln His
 420 425 430

Thr Leu Lys His Phe Glu His Val Arg Met Val Asp Pro Lys Lys Ala
 435 440 445

Ala Gln Ile Arg Ser Gln Val Met Thr His Leu Arg Val Ile Tyr Glu
 450 455 460

Arg Met Asn Gln Ser Leu Ser Leu Leu Tyr Asn Val Pro Ala Val Ala
 465 470 475 480

Glu Glu Ile Gln Asp Glu Val Asp Glu Leu Leu Gln Lys Glu Gln Asn
485 490 495

Tyr Ser Asp Asp Val Leu Ala Asn Met Ile Ser Glu Pro Arg Ile Ser
500 505 510

Tyr Gly Asn Asp Ala Leu Met Pro Ser Leu Thr Glu Thr Lys Thr Thr
515 520 525

Val Glu Leu Leu Pro Val Asn Gly Glu Phe Ser Leu Asp Asp Leu Gln
530 535 540

Pro Trp His Ser Phe Gly Ala Asp Ser Val Pro Ala Asn Thr Glu Asn
545 550 555 560

Glu Val Glu Pro Val Asp Ala Arg Pro Ala Ala Asp Arg Gly Leu Thr
565 570 575

Thr Arg Pro Gly Ser Gly Leu Thr Asn Ile Lys Thr Glu Glu Ile Ser
580 585 590

Glu Val Lys Met Asp Ala Glu Phe Arg His Asp Ser Gly Tyr Glu Val
595 600 605

His His Gln Lys Leu Val Phe Phe Ala Glu Asp Val Gly Ser Asn Lys
610 615 620

Gly Ala Ile Ile Gly Leu Met Val Gly Gly Val Val Ile Ala Thr Val
625 630 635 640

Ile Val Ile Thr Leu Val Met Leu Lys Lys Lys Gln Tyr Thr Ser Ile
645 650 655

His His Gly Val Val Glu Val Asp Ala Ala Val Thr Pro Glu Glu Arg
660 665 670

His Leu Ser Lys Met Gln Gln Asn Gly Tyr Glu Asn Pro Thr Tyr Lys
675 680 685

Phe Phe Glu Gln Met Gln Asn
690 695

<210> 11
<211> 2088
<212> DNA
<213> Homo sapiens

<400> 11
atgctgcccg gtttggcact gctcctgctg gccgcctgga cggctcgggc gctggaggtg 60

cccactgatg	gtaatgctgg	cctgctggct	gaaccccaga	ttgccatggt	ctgtggcaga	120
ctgaacatgc	acatgaatgt	ccagaatggg	aagtgggatt	cagatccatc	agggaccaaa	180
acctgcattg	ataccaagga	aggcatcctg	cagtattgcc	aagaagtcta	ccctgaactg	240
cagatcacca	atgtggtaga	agccaaccaa	ccagtgacca	tccagaactg	gtgcaagcgg	300
ggccgcaagc	agtgaagac	ccatccccac	tttgtgattc	cctaccgctg	cttagttggt	360
gagtttgtaa	gtgatgcctt	tctcgttcct	gacaagtgca	aattcttaca	ccaggagagg	420
atggatgttt	gcgaaactca	tcttcactgg	cacaccgtcg	ccaaagagac	atgcagtgag	480
aagagtacca	acttgcatga	ctacggcatg	ttgctgcctt	gcggaattga	caagttccga	540
ggggtagagt	ttgtgtgttg	cccactggct	gaagaaagtg	acaatgtgga	ttctgctgat	600
gcggaggagg	atgactcgga	tgtctggtgg	ggcggagcag	acacagacta	tgcagatggg	660
agtgaagaca	aagtagtaga	agtagcagag	gaggaagaag	tggctgaggt	ggaagaagaa	720
gaagccgatg	atgacgagga	cgatgaggat	ggtgatgagg	tagaggaaga	ggctgaggaa	780
ccctacgaag	aagccacaga	gagaaccacc	agcattgcc	ccaccaccac	caccaccaca	840
gagtctgtgg	aagaggtggt	togagttcct	acaacagcag	ccagtacccc	tgatgccgtt	900
gacaagtatc	togagacacc	tggggatgag	aatgaacatg	cccatttcca	gaaagccaaa	960
gagaggcttg	aggccaagca	ccgagagaga	atgtcccagg	tcatgagaga	atgggaagag	1020
gcagaacgtc	aagcaagaa	cttgccataa	gctgataaga	aggcagttat	ccagcatttc	1080
caggagaaag	tggaaatcttt	ggaacaggaa	gcagccaacg	agagacagca	gctggtggag	1140
acacacatgg	ccagagtgga	agccatgctc	aatgaccgcc	gcccgcctggc	cctggagaa	1200
tacatcaccg	ctctgcaggc	tgttcctcct	cggcctcgtc	acgtgttcaa	tatgctaaag	1260
aagtatgtcc	gcgcagaaca	gaaggacaga	cagcacacc	taaagcattt	cgagcatgtg	1320
cgcatggtgg	atcccaagaa	agccgctcag	atccggtccc	aggttatgac	acacctccgt	1380
gtgatttatg	agcgcataaa	tcagtctctc	tcctgctctc	acaacgtgcc	tgcagtggcc	1440
gaggagattc	aggatgaagt	tgatgagctg	cttcagaaag	agcaaaacta	ttcagatgac	1500
gtcttgacca	acatgattag	tgaaccaagg	atcagttacg	gaaacgatgc	tctcatgcca	1560
tctttgaccg	aaacgaaaac	caccgtggag	ctccttcccg	tgaatggaga	gttcagcctg	1620
gacgatctcc	agccgtggca	ttcttttggg	gctgactctg	tgccagccaa	caacagaaaac	1680
gaagttgagc	ctgttgatgc	ccgccctgct	gccgaccgag	gactgaccac	tgcaccaggt	1740
tctgggttga	caaatatcaa	gacggaggag	atctctgaag	tgaatctgga	tgcagaattc	1800
cgacatgact	caggatatga	agttcatcat	caaaaattgg	tgttctttgc	agaagatgtg	1860
ggttcaaaca	aaggtgcaat	cattggactc	atggtgggag	gtgttgatcat	agcgacagtg	1920
atcgtcatca	ccttggtgat	gctgaagaag	aaacagtaca	catccattca	tcatggtgtg	1980

gtggaggttg acgccgtgt caccacagag gagcgccacc tgtccaagat gcagcagaac 2040
 ggctacgaaa atccaaccta caagttcttt gagcagatgc agaactag 2088

<210> 12
 <211> 695
 <212> PRT
 <213> Homo sapiens

<400> 12

Met Leu Pro Gly Leu Ala Leu Leu Leu Leu Ala Ala Trp Thr Ala Arg
 1 5 10 15

Ala Leu Glu Val Pro Thr Asp Gly Asn Ala Gly Leu Leu Ala Glu Pro
 20 25 30

Gln Ile Ala Met Phe Cys Gly Arg Leu Asn Met His Met Asn Val Gln
 35 40 45

Asn Gly Lys Trp Asp Ser Asp Pro Ser Gly Thr Lys Thr Cys Ile Asp
 50 55 60

Thr Lys Glu Gly Ile Leu Gln Tyr Cys Gln Glu Val Tyr Pro Glu Leu
 65 70 75 80

Gln Ile Thr Asn Val Val Glu Ala Asn Gln Pro Val Thr Ile Gln Asn
 85 90 95

Trp Cys Lys Arg Gly Arg Lys Gln Cys Lys Thr His Pro His Phe Val
 100 105 110

Ile Pro Tyr Arg Cys Leu Val Gly Glu Phe Val Ser Asp Ala Leu Leu
 115 120 125

Val Pro Asp Lys Cys Lys Phe Leu His Gln Glu Arg Met Asp Val Cys
 130 135 140

Glu Thr His Leu His Trp His Thr Val Ala Lys Glu Thr Cys Ser Glu
 145 150 155 160

Lys Ser Thr Asn Leu His Asp Tyr Gly Met Leu Leu Pro Cys Gly Ile
 165 170 175

Asp Lys Phe Arg Gly Val Glu Phe Val Cys Cys Pro Leu Ala Glu Glu
 180 185 190

Ser Asp Asn Val Asp Ser Ala Asp Ala Glu Glu Asp Asp Ser Asp Val
 195 200 205

Trp Trp Gly Gly Ala Asp Thr Asp Tyr Ala Asp Gly Ser Glu Asp Lys
 210 215 220

Val Val Glu Val Ala Glu Glu Glu Glu Val Ala Glu Val Glu Glu Glu
 225 230 235 240

Glu Ala Asp Asp Asp Glu Asp Asp Glu Asp Gly Asp Glu Val Glu Glu
 245 250 255

Glu Ala Glu Glu Pro Tyr Glu Glu Ala Thr Glu Arg Thr Thr Ser Ile
 260 265 270

Ala Thr Thr Thr Thr Thr Thr Thr Glu Ser Val Glu Glu Val Val Arg
 275 280 285

Val Pro Thr Thr Ala Ala Ser Thr Pro Asp Ala Val Asp Lys Tyr Leu
 290 295 300

Glu Thr Pro Gly Asp Glu Asn Glu His Ala His Phe Gln Lys Ala Lys
 305 310 315 320

Glu Arg Leu Glu Ala Lys His Arg Glu Arg Met Ser Gln Val Met Arg
 325 330 335

Glu Trp Glu Glu Ala Glu Arg Gln Ala Lys Asn Leu Pro Lys Ala Asp
 340 345 350

Lys Lys Ala Val Ile Gln His Phe Gln Glu Lys Val Glu Ser Leu Glu
 355 360 365

Gln Glu Ala Ala Asn Glu Arg Gln Gln Leu Val Glu Thr His Met Ala
 370 375 380

Arg Val Glu Ala Met Leu Asn Asp Arg Arg Arg Leu Ala Leu Glu Asn
 385 390 395 400

Tyr Ile Thr Ala Leu Gln Ala Val Pro Pro Arg Pro Arg His Val Phe
 405 410 415

Asn Met Leu Lys Lys Tyr Val Arg Ala Glu Gln Lys Asp Arg Gln His
 420 425 430

Thr Leu Lys His Phe Glu His Val Arg Met Val Asp Pro Lys Lys Ala
 435 440 445

Ala Gln Ile Arg Ser Gln Val Met Thr His Leu Arg Val Ile Tyr Glu
 450 455 460

Arg Met Asn Gln Ser Leu Ser Leu Leu Tyr Asn Val Pro Ala Val Ala
465 470 475 480

Glu Glu Ile Gln Asp Glu Val Asp Glu Leu Leu Gln Lys Glu Gln Asn
485 490 495

Tyr Ser Asp Asp Val Leu Ala Asn Met Ile Ser Glu Pro Arg Ile Ser
500 505 510

Tyr Gly Asn Asp Ala Leu Met Pro Ser Leu Thr Glu Thr Lys Thr Thr
515 520 525

Val Glu Leu Leu Pro Val Asn Gly Glu Phe Ser Leu Asp Asp Leu Gln
530 535 540

Pro Trp His Ser Phe Gly Ala Asp Ser Val Pro Ala Asn Thr Glu Asn
545 550 555 560

Glu Val Glu Pro Val Asp Ala Arg Pro Ala Ala Asp Arg Gly Leu Thr
565 570 575

Thr Arg Pro Gly Ser Gly Leu Thr Asn Ile Lys Thr Glu Glu Ile Ser
580 585 590

Glu Val Asn Leu Asp Ala Glu Phe Arg His Asp Ser Gly Tyr Glu Val
595 600 605

His His Gln Lys Leu Val Phe Phe Ala Glu Asp Val Gly Ser Asn Lys
610 615 620

Gly Ala Ile Ile Gly Leu Met Val Gly Gly Val Val Ile Ala Thr Val
625 630 635 640

Ile Val Ile Thr Leu Val Met Leu Lys Lys Lys Gln Tyr Thr Ser Ile
645 650 655

His His Gly Val Val Glu Val Asp Ala Ala Val Thr Pro Glu Glu Arg
660 665 670

His Leu Ser Lys Met Gln Gln Asn Gly Tyr Glu Asn Pro Thr Tyr Lys
675 680 685

Phe Phe Glu Gln Met Gln Asn
690 695

<210> 13
 <211> 2088
 <212> DNA
 <213> Homo sapiens

<400> 13

atgctgccccg gtttggcact gctcctgctg gccgcctgga cggctcgggc gctggaggta	60
cccactgatg gtaatgctgg cctgctggct gaaccccaga ttgccatgtt ctgtggcaga	120
ctgaacatgc acatgaatgt ccagaatggg aagtgggatt cagatccatc agggaccaaaa	180
acctgcattg ataccaagga aggcatacctg cagtattgcc aagaagtcta ccctgaactg	240
cagatcacca atgtggtaga agccaaccaa ccagtgacca tccagaactg gtgcaagcgg	300
ggcgcgaagc agtgcaagac ccatacccccac tttgtgattc cctaccgctg cttagttggt	360
gagttttgtaa gtgatgccct tctcgctcct gacaagtga aattcttaca ccaggagagg	420
atggatgttt gcgaaactca tcttcactgg cacaccgtcg ccaaagagac atgcagtgag	480
aagagtacca acttgcatga ctacggcatg ttgctgccct gcggaattga caagttccga	540
ggggtagagt ttgtgtgttg cccactggct gaagaaagtg acaatgtgga ttctgctgat	600
gcggaggagg atgactcgga tgtctggtgg ggcgagcag acacagacta tgcagatggg	660
agtgaagaca aagtagtaga agtagcagag gaggaagaag tggctyaggt ggaagaagaa	720
gaagccgatg atgacgagga cgatgaggat ggtgatgagg tagaggaaga ggctgaggaa	780
ccctacgaag aagccacaga gagaaccacc agcattgcc aaccaccac caccaccaca	840
gagtctgtgg aagaggtggg tcgagttcct acaacagcag ccagtaaccac tgatgccgtt	900
gacaagtatc tcgagacacc tggggatgag aatgaacatg cccatttcca gaaagccaaa	960
gagaggcttg aggccaaagca ccgagagaga atgtcccagg tcatgagaya atgggaagag	1020
gcagaacgtc aagcaaagaa cttgcctaaa gctgataaga aggcagttat ccagcatttc	1080
caggagaaaag tggaatcttt ggaacaggaa gcagccaacg agagacagca gctgggtggag	1140
acacacatgg ccagagtggg agccatgctc aatgaccgcc gccgcctggc cctggagaa	1200
tacatcaccc ctctgcaggc tgttcctcct cggcctcgtc acgtgttcaa tatgctaaag	1260
aagtatgtcc gcgcagaaca gaaggacaga cagcacaccc taaagcattt cgagcatgtg	1320
cgcatggtgg atcccaagaa agccgctcag atccggtccc aggttatgac acacctccgt	1380
gtgatttatg agcgcatgaa tcagtctctc tccctgctct acaacgtgcc tgcagtggcc	1440
gaggagattc aggatgaagt tgatgagctg cttcagaaag agcaaaaacta ttcagatgac	1500
gtcttggcca acatgattag tgaaccaagg atcagttacg gaaacgatgc tctcatgcca	1560
tctttgaccg aaacgaaaac caccgtggag ctcttcccg tgaatggaga gttcagcctg	1620
gacgatctcc agccgtggca ttcttttggg gctgactctg tgccagccaa cacagaaaac	1680
gaagttgagc ctgttgatgc ccgcctgct gccgaccgag gactgaccac tcgaccaggt	1740

tctgggttga caaatatcaa gacggaggag atctctgaag tgaagatgga tgcagaattc 1800
cgacatgact caggatatga agttcatcat caaaaattgg tgttctttgc agaagatgtg 1860
ggttcaaaca aaggtgcaat cattggactc atgggtggcg gtgttgatcat agcgacagtg 1920
atcttcatca ccttggtgat gctgaagaag aaacagtaca catccattca tcatggtgtg 1980
gtggaggttg acgccgctgt caccocagag gagcgccacc tgtccaagat gcagcagaac 2040
ggctacgaaa atccaaccta caagttcttt gagcagatgc agaactag 2088

<210> 14
<211> 695
<212> PRT
<213> Homo sapiens

<400> 14

Met Leu Pro Gly Leu Ala Leu Leu Leu Leu Ala Ala Trp Thr Ala Arg
1 5 10 15

Ala Leu Glu Val Pro Thr Asp Gly Asn Ala Gly Leu Leu Ala Glu Pro
20 25 30

Gln Ile Ala Met Phe Cys Gly Arg Leu Asn Met His Met Asn Val Gln
35 40 45

Asn Gly Lys Trp Asp Ser Asp Pro Ser Gly Thr Lys Thr Cys Ile Asp
50 55 60

Thr Lys Glu Gly Ile Leu Gln Tyr Cys Gln Glu Val Tyr Pro Glu Leu
65 70 75 80

Gln Ile Thr Asn Val Val Glu Ala Asn Gln Pro Val Thr Ile Gln Asn
85 90 95

Trp Cys Lys Arg Gly Arg Lys Gln Cys Lys Thr His Pro His Phe Val
100 105 110

Ile Pro Tyr Arg Cys Leu Val Gly Glu Phe Val Ser Asp Ala Leu Leu
115 120 125

Val Pro Asp Lys Cys Lys Phe Leu His Gln Glu Arg Met Asp Val Cys
130 135 140

Glu Thr His Leu His Trp His Thr Val Ala Lys Glu Thr Cys Ser Glu
145 150 155 160

Lys Ser Thr Asn Leu His Asp Tyr Gly Met Leu Leu Pro Cys Gly Ile
165 170 175

Asp Lys Phe Arg Gly Val Glu Phe Val Cys Cys Pro Leu Ala Glu Glu
 180 185 190

Ser Asp Asn Val Asp Ser Ala Asp Ala Glu Glu Asp Asp Ser Asp Val
 195 200 205

Trp Trp Gly Gly Ala Asp Thr Asp Tyr Ala Asp Gly Ser Glu Asp Lys
 210 215 220

Val Val Glu Val Ala Glu Glu Glu Glu Val Ala Glu Val Glu Glu Glu
 225 230 235 240

Glu Ala Asp Asp Asp Glu Asp Asp Glu Asp Gly Asp Glu Val Glu Glu
 245 250 255

Glu Ala Glu Glu Pro Tyr Glu Glu Ala Thr Glu Arg Thr Thr Ser Ile
 260 265 270

Ala Thr Thr Thr Thr Thr Thr Thr Glu Ser Val Glu Glu Val Val Arg
 275 280 285

Val Pro Thr Thr Ala Ala Ser Thr Pro Asp Ala Val Asp Lys Tyr Leu
 290 295 300

Glu Thr Pro Gly Asp Glu Asn Glu His Ala His Phe Gln Lys Ala Lys
 305 310 315 320

Glu Arg Leu Glu Ala Lys His Arg Glu Arg Met Ser Gln Val Met Arg
 325 330 335

Glu Trp Glu Glu Ala Glu Arg Gln Ala Lys Asn Leu Pro Lys Ala Asp
 340 345 350

Lys Lys Ala Val Ile Gln His Phe Gln Glu Lys Val Glu Ser Leu Glu
 355 360 365

Gln Glu Ala Ala Asn Glu Arg Gln Gln Leu Val Glu Thr His Met Ala
 370 375 380

Arg Val Glu Ala Met Leu Asn Asp Arg Arg Arg Leu Ala Leu Glu Asn
 385 390 395 400

Tyr Ile Thr Ala Leu Gln Ala Val Pro Pro Arg Pro Arg His Val Phe
 405 410 415

Asn Met Leu Lys Lys Tyr Val Arg Ala Glu Gln Lys Asp Arg Gln His
 420 425 430

Thr Leu Lys His Phe Glu His Val Arg Met Val Asp Pro Lys Lys Ala
 435 440 445

Ala Gln Ile Arg Ser Gln Val Met Thr His Leu Arg Val Ile Tyr Glu
 450 455 460

Arg Met Asn Gln Ser Leu Ser Leu Leu Tyr Asn Val Pro Ala Val Ala
 465 470 475 480

Glu Glu Ile Gln Asp Glu Val Asp Glu Leu Leu Gln Lys Glu Gln Asn
 485 490 495

Tyr Ser Asp Asp Val Leu Ala Asn Met Ile Ser Glu Pro Arg Ile Ser
 500 505 510

Tyr Gly Asn Asp Ala Leu Met Pro Ser Leu Thr Glu Thr Lys Thr Thr
 515 520 525

Val Glu Leu Leu Pro Val Asn Gly Glu Phe Ser Leu Asp Asp Leu Gln
 530 535 540

Pro Trp His Ser Phe Gly Ala Asp Ser Val Pro Ala Asn Thr Glu Asn
 545 550 555 560

Glu Val Glu Pro Val Asp Ala Arg Pro Ala Ala Asp Arg Gly Leu Thr
 565 570 575

Thr Arg Pro Gly Ser Gly Leu Thr Asn Ile Lys Thr Glu Glu Ile Ser
 580 585 590

Glu Val Lys Met Asp Ala Glu Phe Arg His Asp Ser Gly Tyr Glu Val
 595 600 605

His His Gln Lys Leu Val Phe Phe Ala Glu Asp Val Gly Ser Asn Lys
 610 615 620

Gly Ala Ile Ile Gly Leu Met Val Gly Gly Val Val Ile Ala Thr Val
 625 630 635 640

Ile Phe Ile Thr Leu Val Met Leu Lys Lys Lys Gln Tyr Thr Ser Ile
 645 650 655

His His Gly Val Val Glu Val Asp Ala Ala Val Thr Pro Glu Glu Arg
 660 665 670

His Leu Ser Lys Met Gln Gln Asn Gly Tyr Glu Asn Pro Thr Tyr Lys
 675 680 685

Phe Phe Glu Gln Met Gln Asn
690 695

<210> 15
<211> 2094
<212> DNA
<213> Homo sapiens

<400> 15
atgctgcccc gtttggcact gctcctgctg gccgcctgga cggctcgggc gctggaggta 60
cccactgatg gtaatgctgg cctgctggct gaaccccaga ttgccatgtt ctgtggcaga 120
ctgaacatgc acatgaatgt ccagaatggg aagtgggatt cagatccatc agggacccaa 180
acctgcattg ataccaagga aggcacctg cagtattgcc aagaagtcta ccctgaactg 240
cagatcacca atgtggtaga agccaaccaa ccagtgaacca tccagaactg gtgcaagcgg 300
ggccgcaagc agtgcaagac ccatcccac tttgtgattc cctaccgctg cttagtgtgt 360
gagtttgtaa gtgatgccct tctcgttcct gacaagtga aattottaca ccaggagagg 420
atggatgttt gcgaaactca tcttcactgg cacaccgtcg ccaaagagac atgcagtga 480
aagagtacca acttgcattg ctacggcatg ttgctgccct gcggaattga caagtccga 540
ggggtagagt ttgtgtgttg cccactggct gaagaaagtg acaatgtgga ttctgctgat 600
ggggaggagg atgactcgga tgtctggtgg ggccgagcag acacagacta tgcagatggg 660
agtgaagaca aagtagtaga agtagcagag gaggaagaag tgyctgaggt ggaagaagaa 720
gaagccgatg atgacgagga cgtatgaggat ggtgatgagg tagagyaaga ggctgaggaa 780
ccctacgaag aagccacaga gagaaccacc agcattgcca ccaccaccac caccaccaca 840
gagtctgtgg aagaggtggt tcgagttcct acaacagcag ccagtacccc tgatgccgtt 900
gaceagtatc tcgagacacc tggggatgag aatgaacatg cccatttcca gaaagccaaa 960
gagaggcttg aggccaaagca ccgagagaga atgtcccagg tcatgagaga atgggaagag 1020
gcagaacgtc aagcaaagaa cttgcctaaa gctgataaga aggcagttat ccagcatttc 1080
caggagaaag tggaatcttt ggaacaggaa gcagccaacg agagacagca gctggtggag 1140
acacacatgg ccagagtgga agccatgctc aatgaccgcc gcegcctggc cctggagaac 1200
tacatcaccg ctctgcaggc tgttcctcct cggcctcgtc acgtgttcaa tatgctaaag 1260
aagtatgtcc gcgcagaaca gaaggacaga cagcacacc taaagcattt cgagcatgtg 1320
cgcatggtgg atcccaagaa agccgctcag atccggtccc aggttatgac acacctccgt 1380
gtgatttatg agcgcattga tcagtctctc tccctgctct acaacgtgcc tgcagtggcc 1440
gaggagattc aggatgaagt tgatgagctg cttcagaaag agcaaaacta ttcagatgac 1500
gtcttgacca acatgattag tgaaccaagg atcagttacg gaaacgatgc tctcatgcca 1560
tctttgaccg aaacgaaaac caccgtggag ctcttcccg tgaatggaga gttcagcctg 1620

gacgatctcc agccgtggca ttcttttggg gctgactctg tgccagccaa cacagaaaac 1680
gaagttgagc ctgttgatgc ccgccctgct gccgaccgag gactgaccac tcgaccaggt 1740
tctgggttga caaatatcaa gacggaggag atctctgaag tgaagatgga tgcagaattc 1800
cgacatgact caggatatga agttcatcat caaaaattgg tgttctttgc agaagatgtg 1860
ggttcaaaca aaggtgcaat cattggactc atggtgggcg gtgttgtcat agcgacagtg 1920
atcgtcatca ccttggtgat gctgaagaag aaacagtaca catccattca tcatggtgtg 1980
gtggaggttg acgccgtgt caccacagag gagcgccacc tgtccaagat gcagcagaac 2040
ggctacgaaa atccaacctt caagttcttt gagcagatgc agaacaagaa gtag 2094

<210> 16
<211> 697
<212> PRT
<213> Homo sapiens

<400> 16

Met Leu Pro Gly Leu Ala Leu Leu Leu Leu Ala Ala Trp Thr Ala Arg
1 5 10 15

Ala Leu Glu Val Pro Thr Asp Gly Asn Ala Gly Leu Leu Ala Glu Pro
20 25 30

Gln Ile Ala Met Phe Cys Gly Arg Leu Asn Met His Met Asn Val Gln
35 40 45

Asn Gly Lys Trp Asp Ser Asp Pro Ser Gly Thr Lys Thr Cys Ile Asp
50 55 60

Thr Lys Glu Gly Ile Leu Gln Tyr Cys Gln Glu Val Tyr Pro Glu Leu
65 70 75 80

Gln Ile Thr Asn Val Val Glu Ala Asn Gln Pro Val Thr Ile Gln Asn
85 90 95

Trp Cys Lys Arg Gly Arg Lys Gln Cys Lys Thr His Pro His Phe Val
100 105 110

Ile Pro Tyr Arg Cys Leu Val Gly Glu Phe Val Ser Asp Ala Leu Leu
115 120 125

Val Pro Asp Lys Cys Lys Phe Leu His Gln Glu Arg Met Asp Val Cys
130 135 140

Glu Thr His Leu His Trp His Thr Val Ala Lys Glu Thr Cys Ser Glu
145 150 155 160

Lys Ser Thr Asn Leu His Asp Tyr Gly Met Leu Leu Pro Cys Gly Ile
 165 170 175

Asp Lys Phe Arg Gly Val Glu Phe Val Cys Cys Pro Leu Ala Glu Glu
 180 185 190

Ser Asp Asn Val Asp Ser Ala Asp Ala Glu Glu Asp Asp Ser Asp Val
 195 200 205

Trp Trp Gly Gly Ala Asp Thr Asp Tyr Ala Asp Gly Ser Glu Asp Lys
 210 215 220

Val Val Glu Val Ala Glu Glu Glu Glu Val Ala Glu Val Glu Glu Glu
 225 230 235 240

Glu Ala Asp Asp Asp Glu Asp Asp Glu Asp Gly Asp Glu Val Glu Glu
 245 250 255

Glu Ala Glu Glu Pro Tyr Glu Glu Ala Thr Glu Arg Thr Thr Ser Ile
 260 265 270

Ala Thr Thr Thr Thr Thr Thr Thr Glu Ser Val Glu Glu Val Val Arg
 275 280 285

Val Pro Thr Thr Ala Ala Ser Thr Pro Asp Ala Val Asp Lys Tyr Leu
 290 295 300

Glu Thr Pro Gly Asp Glu Asn Glu His Ala His Phe Gln Lys Ala Lys
 305 310 315 320

Glu Arg Leu Glu Ala Lys His Arg Glu Arg Met Ser Gln Val Met Arg
 325 330 335

Glu Trp Glu Glu Ala Glu Arg Gln Ala Lys Asn Leu Pro Lys Ala Asp
 340 345 350

Lys Lys Ala Val Ile Gln His Phe Gln Glu Lys Val Glu Ser Leu Glu
 355 360 365

Gln Glu Ala Ala Asn Glu Arg Gln Gln Leu Val Glu Thr His Met Ala
 370 375 380

Arg Val Glu Ala Met Leu Asn Asp Arg Arg Arg Leu Ala Leu Glu Asn
 385 390 395 400

Tyr Ile Thr Ala Leu Gln Ala Val Pro Pro Arg Pro Arg His Val Phe
 405 410 415

Asn Met Leu Lys Lys Tyr Val Arg Ala Glu Gln Lys Asp Arg Gln His
 420 425 430

Thr Leu Lys His Phe Glu His Val Arg Met Val Asp Pro Lys Lys Ala
 435 440 445

Ala Gln Ile Arg Ser Gln Val Met Thr His Leu Arg Val Ile Tyr Glu
 450 455 460

Arg Met Asn Gln Ser Leu Ser Leu Leu Tyr Asn Val Pro Ala Val Ala
 465 470 475 480

Glu Glu Ile Gln Asp Glu Val Asp Glu Leu Leu Gln Lys Glu Gln Asn
 485 490 495

Tyr Ser Asp Asp Val Leu Ala Asn Met Ile Ser Glu Pro Arg Ile Ser
 500 505 510

Tyr Gly Asn Asp Ala Leu Met Pro Ser Leu Thr Glu Thr Lys Thr Thr
 515 520 525

Val Glu Leu Leu Pro Val Asn Gly Glu Phe Ser Leu Asp Asp Leu Gln
 530 535 540

Pro Trp His Ser Phe Gly Ala Asp Ser Val Pro Ala Asn Thr Glu Asn
 545 550 555 560

Glu Val Glu Pro Val Asp Ala Arg Pro Ala Ala Asp Arg Gly Leu Thr
 565 570 575

Thr Arg Pro Gly Ser Gly Leu Thr Asn Ile Lys Thr Glu Glu Ile Ser
 580 585 590

Glu Val Lys Met Asp Ala Glu Phe Arg His Asp Ser Gly Tyr Glu Val
 595 600 605

His His Gln Lys Leu Val Phe Phe Ala Glu Asp Val Gly Ser Asn Lys
 610 615 620

Gly Ala Ile Ile Gly Leu Met Val Gly Gly Val Val Ile Ala Thr Val
 625 630 635 640

Ile Val Ile Thr Leu Val Met Leu Lys Lys Lys Gln Tyr Thr Ser Ile
 645 650 655

His His Gly Val Val Glu Val Asp Ala Ala Val Thr Pro Glu Glu Arg
 660 665 670

His Leu Ser Lys Met Gln Gln Asn Gly Tyr Glu Asn Pro Thr Tyr Lys
675 680 685

Phe Phe Glu Gln Met Gln Asn Lys Lys
690 695

<210> 17
<211> 2094
<212> DNA
<213> Homo sapiens

<400> 17
atgctgcccc gtttggaact gctcctgctg gccgcctgga cggctcgggc gctggaggta 60
cccaactgatg gtaatgctgg cctgctggct gaaccccaga ttgcatgtt ctgtggcaga 120
ctgaacatgc acatgaatgt ccagaatggg aagtgggatt cagatccatc agggaccaaa 180
acctgcattg ataccaagga aggcacctg cagtattgcc aagaagtcta cctgaactg 240
cagatcacca atgtggtaga agccaaccaa ccagtacca tcagaactg gtgcaagcgg 300
ggccgcaagc agtgcaagac ccatcccccac tttgtgattc cctaccgctg cttagtgtgt 360
gagtttgtaa gtgatgcct tctcgttcct gacaagtga aattcttaca ccaggagagg 420
atggatgttt gcgaaactca tcttcactgg cacaccgtcg ccaaagagac atgcaagtga 480
aagagtacca acttgcatga ctacggcatg ttgctgcct gccgaattga caagttccga 540
ggggtagagt ttgtgtgttg cccactggct gaagaaagtg acaatgtgga ttctgctgat 600
gggaggagg atgactcgga tgtctgggtg ggcgagcag acacagaacta tgcagatggg 660
agtgaagaca aagtagtaga agtagcagag gaggaagaag tggctgaggt ggaagaaraa 720
gaagccgatg atgacgagga cgatgaggat ggtgatgagg tagaggaaga ggctgaggaa 780
ccctacgaag aagccacaga gagaaccacc agcattgcaa ccaccaccac caccaccaca 840
gagtctgtgg aagaggtggt tcgagttcct acaacagcag ccagtacccc tgatgccgtt 900
gacaagtatc tcgagacacc tggggatgag aatgaacatg cccatttcca gaaagccaaa 960
gagaggcttg aggccaaagca ccgagagaga atgtcccagg tcatgagaga atgggaagag 1020
gcagaacgtc aagcaaagaa cttgcctaaa gctgataaga aggcagttat ccagcatttc 1080
caggagaaag tggaatcttt ggaacaggaa gcagccaacg agagacagca gctggtggag 1140
acacacatgg ccagagtgga agccatgctc aatgaccgcc gccgcctggc cctggagaac 1200
tacatcaccg ctctgcaggc tggttcctcct cggcctcgtc acgtgttcaa tatgctaaag 1260
aagtatgtcc gcgcagaaca gaaggacaga cagcacacc taaagcattt cgagcatgtg 1320
cgcatggtgg atcccaagaa agccgctcag atccggtccc aggttatgac acacctccgt 1380
gtgatttatg agcgcataaa tcagtctctc tcctgtctc acaacgtgcc tgcagtggcc 1440
gaggagattc aggatgaagt tgatgagctg cttcagaaag agcaaaacta ttcagatgac 1500

gtcttggcca acatgattag tgaaccaagg atcagttacg gaaacgatgc tetcatgcca 1560
tctttgaccg aaacgaaaac caccgtggag ctccctccccg tgaatggaga gttcagcctg 1620
gacgatctcc agccgtggca ttcttttggg gctgactctg tgccagccaa cacagaaaac 1680
gaagttgagc ctgttgatgc ccgccctgct gccgaccgag gactgaccac tcgaccaggt 1740
tctgggttga caaatatcaa gacggaggag atctctgaag tgaatctgga tgcagaattc 1800
cgacatgact caggatatga agttcatcat caaaaattgg tgttctttgc agaagatgtg 1860
ggttcaaaca aaggtgcaat cattggactc atggtgggcg gtgttgatcat agcgacagtg 1920
atcgicacat ccttggtgat gctgaagaag aaacagtaca catccattca tcatggtgtg 1980
gtggagggtg acgccgctgt caccocagag gagcgccacc tgtccaagat gcagcagaac 2040
ggctacgaaa atccaacctt caagttcttt gagcagatgc agaacaagaa gttag 2094

<210> 18
<211> 697
<212> PRT
<213> Homo sapiens

<400> 18

Met Leu Pro Gly Leu Ala Leu Leu Leu Leu Ala Ala Trp Thr Ala Arg
1 5 10 15

Ala Leu Glu Val Pro Thr Asp Gly Asn Ala Gly Leu Leu Ala Glu Pro
20 25 30

Gln Ile Ala Met Phe Cys Gly Arg Leu Asn Met His Met Asn Val Gln
35 40 45

Asn Gly Lys Trp Asp Ser Asp Pro Ser Gly Thr Lys Thr Cys Ile Asp
50 55 60

Thr Lys Glu Gly Ile Leu Gln Tyr Cys Gln Glu Val Tyr Pro Gly Leu
65 70 75 80

Gln Ile Thr Asn Val Val Glu Ala Asn Gln Pro Val Thr Ile Gln Asn
85 90 95

Trp Cys Lys Arg Gly Arg Lys Gln Cys Lys Thr His Pro His Phe Val
100 105 110

Ile Pro Tyr Arg Cys Leu Val Gly Glu Phe Val Ser Asp Ala Leu Leu
115 120 125

Val Pro Asp Lys Cys Lys Phe Leu His Gln Glu Arg Met Asp Val Cys
130 135 140

Glu Thr His Leu His Trp His Thr Val Ala Lys Glu Thr Cys Ser Glu
 145 150 155 160
 Lys Ser Thr Asn Leu His Asp Tyr Gly Met Leu Leu Pro Cys Gly Ile
 165 170 175
 Asp Lys Phe Arg Gly Val Glu Phe Val Cys Cys Pro Leu Ala Glu Glu
 180 185 190
 Ser Asp Asn Val Asp Ser Ala Asp Ala Glu Glu Asp Asp Ser Asp Val
 195 200 205
 Trp Trp Gly Gly Ala Asp Thr Asp Tyr Ala Asp Gly Ser Glu Asp Lys
 210 215 220
 Val Val Glu Val Ala Glu Glu Glu Val Ala Glu Val Glu Glu Glu
 225 230 235 240
 Glu Ala Asp Asp Asp Glu Asp Asp Glu Asp Gly Asp Glu Val Glu Glu
 245 250 255
 Glu Ala Glu Glu Pro Tyr Glu Glu Ala Thr Glu Arg Thr Thr Ser Ile
 260 265 270
 Ala Thr Thr Thr Thr Thr Thr Thr Glu Ser Val Glu Glu Val Val Arg
 275 280 285
 Val Pro Thr Thr Ala Ala Ser Thr Pro Asp Ala Val Asp Lys Tyr Leu
 290 295 300
 Glu Thr Pro Gly Asp Glu Asn Glu His Ala His Phe Gln Lys Ala Lys
 305 310 315 320
 Glu Arg Leu Glu Ala Lys His Arg Glu Arg Met Ser Gln Val Met Arg
 325 330 335
 Glu Trp Glu Glu Ala Glu Arg Gln Ala Lys Asn Leu Pro Lys Ala Asp
 340 345 350
 Lys Lys Ala Val Ile Gln His Phe Gln Glu Lys Val Glu Ser Leu Glu
 355 360 365
 Gln Glu Ala Ala Asn Glu Arg Gln Gln Leu Val Glu Thr His Met Ala
 370 375 380
 Arg Val Glu Ala Met Leu Asn Asp Arg Arg Arg Leu Ala Leu Glu Asn
 385 390 395 400

Tyr Ile Thr Ala Leu Gln Ala Val Pro Pro Arg Pro Arg His Val Phe
 405 410 415

Asn Met Leu Lys Lys Tyr Val Arg Ala Glu Gln Lys Asp Arg Gln His
 420 425 430

Thr Leu Lys His Phe Glu His Val Arg Met Val Asp Pro Lys Lys Ala
 435 440 445

Ala Gln Ile Arg Ser Gln Val Met Thr His Leu Arg Val Ile Tyr Glu
 450 455 460

Arg Met Asn Gln Ser Leu Ser Leu Leu Tyr Asn Val Pro Ala Val Ala
 465 470 475 480

Glu Glu Ile Gln Asp Glu Val Asp Glu Leu Leu Gln Lys Glu Gln Asn
 485 490 495

Tyr Ser Asp Asp Val Leu Ala Asn Met Ile Ser Glu Pro Arg Ile Ser
 500 505 510

Tyr Gly Asn Asp Ala Leu Met Pro Ser Leu Thr Glu Thr Lys Thr Thr
 515 520 525

Val Glu Leu Leu Pro Val Asn Gly Glu Phe Ser Leu Asp Asp Leu Gln
 530 535 540

Pro Trp His Ser Phe Gly Ala Asp Ser Val Pro Ala Asn Thr Glu Asn
 545 550 555 560

Glu Val Glu Pro Val Asp Ala Arg Pro Ala Ala Asp Arg Gly Leu Thr
 565 570 575

Thr Arg Pro Gly Ser Gly Leu Thr Asn Ile Lys Thr Glu Glu Ile Ser
 580 585 590

Glu Val Asn Leu Asp Ala Glu Phe Arg His Asp Ser Gly Tyr Glu Val
 595 600 605

His His Gln Lys Leu Val Phe Phe Ala Glu Asp Val Gly Ser Asn Lys
 610 615 620

Gly Ala Ile Ile Gly Leu Met Val Gly Gly Val Val Ile Ala Thr Val
 625 630 635 640

Ile Val Ile Thr Leu Val Met Leu Lys Lys Lys Gln Tyr Thr Ser Ile
 645 650 655

His His Gly Val Val Glu Val Asp Ala Ala Val Thr Pro Glu Glu Arg
660 665 670

His Leu Ser Lys Met Gln Gln Asn Gly Tyr Glu Asn Pro Thr Tyr Lys
675 680 685

Phe Phe Glu Gln Met Gln Asn Lys Lys
690 695

<210> 19
<211> 2094
<212> DNA
<213> Homo sapiens

<400> 19
atgctgcccg gtttggcact gtcctgctg gccgctgga cggctcgggc gctggaggta 60
cccactgatg gtaatgcttg cctgctgget gaaccccaga ttgccatgtt ctgtggcaga 120
ctgaacatgc acatgaatgt ccagaatggg aagtgggatt cagatccatc agggacacaa 180
acctgcattg ataccaagga aggcacctcg cagtattgcc aagaagtcta cctgaactg 240
cagatcacca atgtggtaga agccaaccaa ccagtaccca tccagaactg gtgcaagcgg 300
ggccgcaagc agtgcaagac ccaccccccac tttgtgatcc cctaccgctg cttagtgtgt 360
gagtttgtaa gtgatgcctt tctcgttcct gacaagtcca aattcttaca ccaggagagg 420
atggatgttt gcgaaactca tcttcaactgg cacaccgtcg ccaaagagac atgcagttag 480
aagagtacca acttgcatga ctacggcatg ttgctgcctt gcggaattga caagtccga 540
ggggtagagt ttgtgtgttg cccactggct gaagaaagtg acaatgtgga ttctgctgat 600
gcggaggagg atgactcgga tgtctggtgg gcgggagcag acacagacta tgcagatggg 660
agtgaagaca aagtagtaga agtagcagag gaggaagaag tggctgaggt ggaagaagaa 720
gaagccgatg atgacgagga cgatgaggat ggtgatgagg tagaggaaga ggctgaggaa 780
ccctacgaag aagccacaga gagaaccacc agcattgcca ccaccaccac caccaccaca 840
gagtctgtgg aagaggtggt tcgagttcct acaacagcag ccagtacccc tgatgccgtt 900
gacaagtatc tcgagacacc tggggatgag aatgaacatg ccattttcca gaaagccaaa 960
gagaggcttg aggccaagca ccgagagaga atgtcccagg tcatgagaga atgggaagag 1020
gcagaacgtc aagcaaagaa cttgcctaaa gctgataaga aggcagttat ccagcatttc 1080
caggagaaag tggaatcttt ggaacaggaa gcagccaacg agagacagca gctggtggag 1140
acacacatgg ccagagtgga agccatgctc aatgaccgcc gccgctggc cctggagaac 1200
tacatcaccg ctctgcaggc tgttcctcct cggcctcgtc acgtgttcaa tatgctaaag 1260
aagtatgtcc gcgcagaaca gaaggacaga cagcacaccc taaagcattt cgagcatgtg 1320
cgcatggtgg atcccaagaa agccgctcag atccggtccc aggttatgac acacctccgt 1380

gtgatttatg agcgcatgaa tcagtctctc tccctgctct acaacgtgcc tgcagtggcc 1440
 gaggagattc aggatgaagt tgatgagctg cttcagaaag agcaaaacta ttcagatgac 1500
 gtcttggcca acatgattag tgaaccaagg atcagttacg gaaacgatgc tctcatgcca 1560
 tctttgaccg aaacgaaaac caccgtggag ctcttcccg tgaatggaga gttcagcctg 1620
 gacgatctcc agccgtggca ttcttttggg gctgactctg tgccagccaa cacagaaaac 1680
 gaagttgagc ctgttgatgc ccgccctgct gccgaccgag gactgaccac tcgaccaggt 1740
 tctgggttga caaatatcaa gacggaggag atctctgaag tgaagatgga tgcagaattc 1800
 cgacatgact caggatatga agttcatcat caaaaattgg tgttctttgc agaagatgtg 1860
 ggttcaaaca aaggtgcaat cattggactc atggtgggcg gtgttgatcat agcgacagtg 1920
 atcttcatca ccttggtgat gctgaagaag aaacagtaca catccattca tcatggtgtg 1980
 gtggaggttg acgccgctgt caccacagag gagcgccacc tgtccaagtat gcagcagaac 2040
 ggtacgaaa atccaacctt caagttcttt gacgagatgc agaacaagaa gtag 2094

<210> 20
 <211> 697
 <212> PRT
 <213> Homo sapiens

<400> 20

Met Leu Pro Gly Leu Ala Leu Leu Leu Ala Ala Trp Thr Ala Arg
1 5 10 15

Ala Leu Glu Val Pro Thr Asp Gly Asn Ala Gly Leu Leu Ala Glu Pro
20 25 30

Gln Ile Ala Met Phe Cys Gly Arg Leu Asn Met His Met Asn Val Gln
35 40 45

Asn Gly Lys Trp Asp Ser Asp Pro Ser Gly Thr Lys Thr Cys Ile Asp
50 55 60

Thr Lys Glu Gly Ile Leu Gln Tyr Cys Gln Glu Val Tyr Pro Glu Leu
65 70 75 80

Gln Ile Thr Asn Val Val Glu Ala Asn Gln Pro Val Thr Ile Gln Asn
85 90 95

Trp Cys Lys Arg Gly Arg Lys Gln Cys Lys Thr His Pro His Phe Val
100 105 110

Ile Pro Tyr Arg Cys Leu Val Gly Glu Phe Val Ser Asp Ala Leu Leu
115 120 125

Val Pro Asp Lys Cys Lys Phe Leu His Gln Glu Arg Met Asp Val Cys
 130 135 140

Glu Thr His Leu His Trp His Thr Val Ala Lys Glu Thr Cys Ser Glu
 145 150 155 160

Lys Ser Thr Asn Leu His Asp Tyr Gly Met Leu Leu Pro Cys Gly Ile
 165 170 175

Asp Lys Phe Arg Gly Val Glu Phe Val Cys Cys Pro Leu Ala Glu Glu
 180 185 190

Ser Asp Asn Val Asp Ser Ala Asp Ala Glu Glu Asp Asp Ser Asp Val
 195 200 205

Trp Trp Gly Gly Ala Asp Thr Asp Tyr Ala Asp Gly Ser Glu Asp Lys
 210 215 220

Val Val Glu Val Ala Glu Glu Glu Glu Val Ala Glu Val Glu Glu Glu
 225 230 235 240

Glu Ala Asp Asp Asp Glu Asp Asp Glu Asp Gly Asp Glu Val Glu Glu
 245 250 255

Glu Ala Glu Glu Pro Tyr Glu Glu Ala Thr Glu Arg Thr Thr Ser Ile
 260 265 270

Ala Thr Thr Thr Thr Thr Thr Thr Glu Ser Val Glu Glu Val Val Arg
 275 280 285

Val Pro Thr Thr Ala Ala Ser Thr Pro Asp Ala Val Asp Lys Tyr Leu
 290 295 300

Glu Thr Pro Gly Asp Glu Asn Glu His Ala His Phe Gln Lys Ala Lys
 305 310 315 320

Glu Arg Leu Glu Ala Lys His Arg Glu Arg Met Ser Gln Val Met Arg
 325 330 335

Glu Trp Glu Glu Ala Glu Arg Gln Ala Lys Asn Leu Pro Lys Ala Asp
 340 345 350

Lys Lys Ala Val Ile Gln His Phe Gln Glu Lys Val Glu Ser Leu Glu
 355 360 365

Gln Glu Ala Ala Asn Glu Arg Gln Gln Leu Val Glu Thr His Met Ala
 370 375 380

Arg Val Glu Ala Met Leu Asn Asp Arg Arg Arg Leu Ala Leu Glu Asn
 385 390 395 400

Tyr Ile Thr Ala Leu Gln Ala Val Pro Pro Arg Pro Arg His Val Phe
 405 410 415

Asn Met Leu Lys Lys Tyr Val Arg Ala Glu Gln Lys Asp Arg Gln His
 420 425 430

Thr Leu Lys His Phe Glu His Val Arg Met Val Asp Pro Lys Lys Ala
 435 440 445

Ala Gln Ile Arg Ser Gln Val Met Thr His Leu Arg Val Ile Tyr Glu
 450 455 460

Arg Met Asn Gln Ser Leu Ser Leu Leu Tyr Asn Val Pro Ala Val Ala
 465 470 475 480

Glu Glu Ile Gln Asp Glu Val Asp Glu Leu Leu Gln Lys Glu Gln Asn
 485 490 495

Tyr Ser Asp Asp Val Leu Ala Asn Met Ile Ser Glu Pro Arg Ile Ser
 500 505 510

Tyr Gly Asn Asp Ala Leu Met Pro Ser Leu Thr Glu Thr Lys Thr Thr
 515 520 525

Val Glu Leu Leu Pro Val Asn Gly Glu Phe Ser Leu Asp Asp Leu Gln
 530 535 540

Pro Trp His Ser Phe Gly Ala Asp Ser Val Pro Ala Asn Thr Glu Asn
 545 550 555 560

Glu Val Glu Pro Val Asp Ala Arg Pro Ala Ala Asp Arg Gly Leu Thr
 565 570 575

Thr Arg Pro Gly Ser Gly Leu Thr Asn Ile Lys Thr Glu Glu Ile Ser
 580 585 590

Glu Val Lys Met Asp Ala Glu Phe Arg His Asp Ser Gly Tyr Glu Val
 595 600 605

His His Gln Lys Leu Val Phe Phe Ala Glu Asp Val Gly Ser Asn Lys
 610 615 620

Gly Ala Ile Ile Gly Leu Met Val Gly Gly Val Val Ile Ala Thr Val
 625 630 635 640

Ile Phe Ile Thr Leu Val Met Leu Lys Lys Lys Gln Tyr Thr Ser Ile
645 650 655

His His Gly Val Val Glu Val Asp Ala Ala Val Thr Pro Glu Glu Arg
660 665 670

His Leu Ser Lys Met Gln Gln Asn Gly Tyr Glu Asn Pro Thr Tyr Lys
675 680 685

Phe Phe Glu Gln Met Gln Asn Lys Lys
690 695

<210> 21
<211> 1341
<212> DNA
<213> Homo sapiens

<400> 21
atggctagca tgactggtgg acagcaaattg ggtcgcggat ccaccagca cggcatccgg 60
ctgcccctgc gcagcggcct ggggggcgcc cccctggggc tgcggctgcc ccgggagacc 120
gacgaagagc ccgaggagcc cggccggagg ggcagctttg tggagatggt ggacaacctg 180
aggggcaagt cggggcaggg ctactacgtg gagatgaccg tgggcagccc ccgcagacg 240
ctcaacatcc tgggtggatac aggcagcagt aactttgcag tgggtgctgc cccccacccc 300
ttctgcatc gctactacca gaggcagctg tccagcacat accgggacct ccggaagggt 360
gtgtatgtgc cctacacca gggcaagtgg gaaggggagc tgggcaccga cctggtaagc 420
atcccccatg gcccacagt cactgtgcgt gccaacattg ctgccatcac tgaatcagac 480
aagttcttca tcaacggctc caactgggaa ggcacacctg ggctggccta tgetgagatt 540
gccaggcctg acgactccct ggagcctttc ttgactctc tggtaaagca gaccacagtt 600
cccaacctct tctccctgca cttttgtggt gctggcttcc cctcaacca gtctgaagtg 660
ctggcctctg tcggagggag catgatcatt ggaggtatcg accactcgt gtacacaggc 720
agtctctggt atacacccat ccggcgggag tggattatg aggtcatcat tgtgcgggtg 780
gagatcaatg gacaggatct gaaaatggac tgcaaggagt acaactatga caagagcatt 840
gtggacagtg gcaccacca ccttcgtttg cccaagaaag tgtttgaagc tgcagtcaaa 900
tccatcaagg cagcctctc cacggagaag ttccctgatg gtttctggct aggagagcag 960
ctggtgtgct ggcaagcagg caccaccct tggaaacatt tccagtcac ctactctac 1020
ctaattgggtg aggttaccaa ccagtccttc cgcacacca tcttccgca gcaataacctg 1080
cggccagtgg aagatgtggc cagtcacca gacgactgtt acaagtttgc catctcacag 1140
tcatccacgg gcaactgtat gggagctgtt atcatggagg gcttctacgt tgtctttgat 1200
cgggcccga aacgaattgg ctttgctgtc agcgcttgcc atgtgcacga tgagttcagg 1260

acggcagcgg tggaaggccc tttgtcacc ttggacatgg aagactgtgg ctacaacatt 1320
ccacagacag atgagtcatg a 1341

<210> 22
<211> 446
<212> PRT
<213> Homo sapiens

<400> 22

Met Ala Ser Met Thr Gly Gly Gln Gln Met Gly Arg Gly Ser Thr Gln
1 5 10 15

His Gly Ile Arg Leu Pro Leu Arg Ser Gly Leu Gly Gly Ala Pro Leu
20 25 30

Gly Leu Arg Leu Pro Arg Glu Thr Asp Glu Glu Pro Glu Glu Pro Gly
35 40 45

Arg Arg Gly Ser Phe Val Glu Met Val Asp Asn Leu Arg Gly Lys Ser
50 55 60

Gly Gln Gly Tyr Tyr Val Glu Met Thr Val Gly Ser Pro Pro Gln Thr
65 70 75 80

Leu Asn Ile Leu Val Asp Thr Gly Ser Ser Asn Phe Ala Val Gly Ala
85 90 95

Ala Pro His Pro Phe Leu His Arg Tyr Tyr Gln Arg Gln Leu Ser Ser
100 105 110

Thr Tyr Arg Asp Leu Arg Lys Gly Val Tyr Val Pro Tyr Thr Gln Gly
115 120 125

Lys Trp Glu Gly Glu Leu Gly Thr Asp Leu Val Ser Ile Pro His Gly
130 135 140

Pro Asn Val Thr Val Arg Ala Asn Ile Ala Ala Ile Thr Glu Ser Asp
145 150 155 160

Lys Phe Phe Ile Asn Gly Ser Asn Trp Glu Gly Ile Leu Gly Leu Ala
165 170 175

Tyr Ala Glu Ile Ala Arg Pro Asp Asp Ser Leu Glu Pro Phe Phe Asp
180 185 190

Ser Leu Val Lys Gln Thr His Val Pro Asn Leu Phe Ser Leu His Leu
195 200 205

Cys Gly Ala Gly Phe Pro Leu Asn Gln Ser Glu Val Leu Ala Ser Val
 210 215 220

Gly Gly Ser Met Ile Ile Gly Gly Ile Asp His Ser Leu Tyr Thr Gly
 225 230 235 240

Ser Leu Trp Tyr Thr Pro Ile Arg Arg Glu Trp Tyr Tyr Glu Val Ile
 245 250 255

Ile Val Arg Val Glu Ile Asn Gly Gln Asp Leu Lys Met Asp Cys Lys
 260 265 270

Glu Tyr Asn Tyr Asp Lys Ser Ile Val Asp Ser Gly Thr Thr Asn Leu
 275 280 285

Arg Leu Pro Lys Lys Val Phe Glu Ala Ala Val Lys Ser Ile Lys Ala
 290 295 300

Ala Ser Ser Thr Glu Lys Phe Pro Asp Gly Phe Trp Leu Gly Glu Gln
 305 310 315 320

Leu Val Cys Trp Gln Ala Gly Thr Thr Pro Trp Asn Ile Phe Pro Val
 325 330 335

Ile Ser Leu Tyr Leu Met Gly Glu Val Thr Asn Gln Ser Phe Arg Ile
 340 345 350

Thr Ile Leu Pro Gln Gln Tyr Leu Arg Pro Val Glu Asp Val Ala Thr
 355 360 365

Ser Gln Asp Asp Cys Tyr Lys Phe Ala Ile Ser Gln Ser Ser Thr Gly
 370 375 380

Thr Val Met Gly Ala Val Ile Met Glu Gly Phe Tyr Val Val Phe Asp
 385 390 395 400

Arg Ala Arg Lys Arg Ile Gly Phe Ala Val Ser Ala Cys His Val His
 405 410 415

Asp Glu Phe Arg Thr Ala Ala Val Glu Gly Pro Phe Val Thr Leu Asp
 420 425 430

Met Glu Asp Cys Gly Tyr Asn Ile Pro Gln Thr Asp Glu Ser
 435 440 445

<210> 23
 <211> 1380
 <212> DNA
 <213> Homo sapiens

<400> 23
 atggctagca tgactggtgg acagcaaata ggtcgcggat cgatgactat ctctgactct 60
 ccgcgtgaac aggacggatc caccacgac ggcacccggc tgccctcgcg cagcggcctg 120
 gggggcgccc ccctgggggt gcggtgccc cgggagaccg acgaagagcc cgaggagccc 180
 ggccggaggg gcagctttgt ggagatggtg gacaacctga ggggcaagtc ggggcagggc 240
 tactacgtgg agatgaccgt gggcagcccc ccgcagacgc tcaacatcct ggtggataca 300
 ggcagcagta actttgcagt ggggtgctgcc cccacccctt tctgcatcg ctactaccag 360
 aggcagctgt ccagcacata ccgggacctc cggaagggtg tgtatgtgcc ctacaccag 420
 ggcaagtggg aaggggagct gggcaccgac ctggtgaagca tcccccatgg cccaacgctc 480
 actgtgctg ccaacattgc tgccatcact gaatcagaca agttcttcat caacggctcc 540
 aactgggaag gcatcctggg gctggcctat gctgagattg ccaggcctga cgactccctg 600
 gagcctttct ttgactctct ggtaaagcag acccacgttc ccaacctctt ctccctgcac 660
 ctttgtggtg ctggcttccc cctcaaccag tctgaagtgc tggcctctgt cggaggggagc 720
 atgatcattg gaggtatcga ccaactcgctg tacacaggca gtctctggta tacacccatc 780
 cggcgggagt ggtattatga ggtcatcatt gtgcgggtgg agatcaatgg acaggatctg 840
 aaaatggact gcaaggagta caactatgac aagagcattg tggacagtgg caccaccaac 900
 cttcgtttgc ccaagaaagt gtttgaagct gcagtcaaat ccatcaaggc agcctcctcc 960
 acggagaagt tccctgatgg tttctggcta ggagagcagc tgggtgtgctg gcaagcaggc 1020
 accaccctt ggaacatttt ccagtcac tcaactctacc taatgggtga ggttaccaac 1080
 cagtccttcc gcatcaccat ccttccgcag caatacctgc ggccagtgga agatgtggcc 1140
 acgtccaag acgactgtta caagtttgcc atctcacagt catccacggg cactgttatg 1200
 ggagctgtta tcatggaggg cttctacgtt gtctttgatc gggcccgaaa acgaattggc 1260
 tttgctgtca gcgcttgcca tgtgcacgat gagttcagga cggcagcggg ggaaggccct 1320
 tttgtcacct tggacatgga agactgtggc tacaacattc cacagacaga tgagtcatga 1380

<210> 24
 <211> 459
 <212> PRT
 <213> Homo sapiens

<400> 24

Met	Ala	Ser	Met	Thr	Gly	Gly	Gln	Gln	Met	Gly	Arg	Gly	Ser	Met	Thr
1				5					10					15	

Ile Ser Asp Ser Pro Arg Glu Gln Asp Gly Ser Thr Gln His Gly Ile
 20 25 30

Arg Leu Pro Leu Arg Ser Gly Leu Gly Gly Ala Pro Leu Gly Leu Arg
 35 40 45

Leu Pro Arg Glu Thr Asp Glu Glu Pro Glu Glu Pro Gly Arg Arg Gly
 50 55 60

Ser Phe Val Glu Met Val Asp Asn Leu Arg Gly Lys Ser Gly Gln Gly
 65 70 75 80

Tyr Tyr Val Glu Met Thr Val Gly Ser Pro Pro Gln Thr Leu Asn Ile
 85 90 95

Leu Val Asp Thr Gly Ser Ser Asn Phe Ala Val Gly Ala Ala Pro His
 100 105 110

Pro Phe Leu His Arg Tyr Tyr Gln Arg Gln Leu Ser Ser Thr Tyr Arg
 115 120 125

Asp Leu Arg Lys Gly Val Tyr Val Pro Tyr Thr Gln Gly Lys Trp Glu
 130 135 140

Gly Glu Leu Gly Thr Asp Leu Val Ser Ile Pro His Gly Pro Asn Val
 145 150 155 160

Thr Val Arg Ala Asn Ile Ala Ala Ile Thr Glu Ser Asp Lys Phe Phe
 165 170 175

Ile Asn Gly Ser Asn Trp Glu Gly Ile Leu Gly Leu Ala Tyr Ala Glu
 180 185 190

Ile Ala Arg Pro Asp Asp Ser Leu Glu Pro Phe Phe Asp Ser Leu Val
 195 200 205

Lys Gln Thr His Val Pro Asn Leu Phe Ser Leu His Leu Cys Gly Ala
 210 215 220

Gly Phe Pro Leu Asn Gln Ser Glu Val Leu Ala Ser Val Gly Gly Ser
 225 230 235 240

Met Ile Ile Gly Gly Ile Asp His Ser Leu Tyr Thr Gly Ser Leu Trp
 245 250 255

Tyr Thr Pro Ile Arg Arg Glu Trp Tyr Tyr Glu Val Ile Ile Val Arg
 260 265 270

Val Glu Ile Asn Gly Gln Asp Leu Lys Met Asp Cys Lys Glu Tyr Asn
 275 280 285
 Tyr Asp Lys Ser Ile Val Asp Ser Gly Thr Thr Asn Leu Arg Leu Pro
 290 295 300
 Lys Lys Val Phe Glu Ala Ala Val Lys Ser Ile Lys Ala Ala Ser Ser
 305 310 315 320
 Thr Glu Lys Phe Pro Asp Gly Phe Trp Leu Gly Glu Gln Leu Val Cys
 325 330 335
 Trp Gln Ala Gly Thr Thr Pro Trp Asn Ile Phe Pro Val Ile Ser Leu
 340 345 350
 Tyr Leu Met Gly Glu Val Thr Asn Gln Ser Phe Arg Ile Thr Ile Leu
 355 360 365
 Pro Gln Gln Tyr Leu Arg Pro Val Glu Asp Val Ala Thr Ser Gln Asp
 370 375 380
 Asp Cys Tyr Lys Phe Ala Ile Ser Gln Ser Ser Thr Gly Thr Val Met
 385 390 395 400
 Gly Ala Val Ile Met Glu Gly Phe Tyr Val Val Phe Asp Arg Ala Arg
 405 410 415
 Lys Arg Ile Gly Phe Ala Val Ser Ala Cys His Val His Asp Glu Phe
 420 425 430
 Arg Thr Ala Ala Val Glu Gly Pro Phe Val Thr Leu Asp Met Glu Asp
 435 440 445
 Cys Gly Tyr Asn Ile Pro Gln Thr Asp Glu Ser
 450 455

<210> 25

<211> 1302

<212> DNA

<213> Homo sapiens

<400> 25

atgactcagc atggtattcg tctgccactg cgtagcggtc tgggtggtgc tccactgggt	60
ctgcgtctgc cccgggagac cgacgaagag cccgaggagc ccggccggag gggcagcttt	120
gtggagatgg tggacaacct gaggggcaag tcggggcagg gctactacgt ggagatgacc	180
gtgggcagcc ccccgagac gctcaacatc ctggtggata caggcagcag taactttgca	240
gtgggtgctg cccccaccc cttoctgcat cgctactacc agaggcagct gtccagcaca	300

taccgggacc tccggaaggg tgtgtatgtg ccctacaccc agggcaagtg ggaaggggag	360
ctgggacccg acctggtaag catcccccat ggccccaacg tcaactgtgcg tgccaacatt	420
gctgccatca ctgaatcaga caagttcttc atcaacggct ccaactggga aggcatcctg	480
gggctggcct atgctgagat tgccaggcct gacgactccc tggagccttt ctttgactct	540
ctggtaaagc agaccacagt tcccaacctc ttctccctgc acctttgtgg tgctggcttc	600
cccctcaacc agtctgaagt gctggcctct gtcggaggga gcatgatcat tggaggtatc	660
gaccactcgc tgtacacagg cagtctctgg tatacaccca tccggcggga gtggtattat	720
gaggtcatca ttgtgcggtt ggagatcaat ggacaggatc tgaaaatgga ctgcaaggag	780
tacaactatg acaagagcat tgtggacagt ggcaccacca accttcgttt gcccaagaaa	840
gtgtttgaag ctgcagtcaa atccatcaag gcagcctcct ccacggagaa gttccctgat	900
ggtttctggc taggagagca gctggtgtgc tggcaagcag gcaccacccc ttggaacatt	960
ttcccagtca tctactcta cctaattgggt gaggttacca accagtcctt ccgcatcacc	1020
atccttccgc agcaatacct gcggccagtg gaagatgtgg ccacgtccca agacgactgt	1080
tacaagtttg ccatctcaca gtcattccac ggcaactgtta tgggagctgt tatcatggag	1140
ggcttctacg ttgtctttga tcggggcccga aaacgaattg gctttgctgt cagcgcttgc	1200
catgtgcacg atgagttcag gacggcagcg gtggaaggcc cttttgtcac cttggacatg	1260
gaagactgtg gctacaacat tccacagaca gatgagtcat ga	1302

<210> 26
 <211> 433
 <212> PRT
 <213> Homo sapiens

<400> 26

Met	Thr	Gln	His	Gly	Ile	Arg	Leu	Pro	Leu	Arg	Ser	Gly	Leu	Gly	Gly
1				5					10					15	

Ala	Pro	Leu	Gly	Leu	Arg	Leu	Pro	Arg	Glu	Thr	Asp	Glu	Glu	Pro	Glu
			20					25					30		

Glu	Pro	Gly	Arg	Arg	Gly	Ser	Phe	Val	Glu	Met	Val	Asp	Asn	Leu	Arg
		35					40					45			

Gly	Lys	Ser	Gly	Gln	Gly	Tyr	Tyr	Val	Glu	Met	Thr	Val	Gly	Ser	Pro
	50					55					60				

Pro	Gln	Thr	Leu	Asn	Ile	Leu	Val	Asp	Thr	Gly	Ser	Ser	Asn	Phe	Ala
65					70					75					80

Val Gly Ala Ala Pro His Pro Phe Leu His Arg Tyr Tyr Gln Arg Gln
 85 90 95

Leu Ser Ser Thr Tyr Arg Asp Leu Arg Lys Gly Val Tyr Val Pro Tyr
 100 105 110

Thr Gln Gly Lys Trp Glu Gly Glu Leu Gly Thr Asp Leu Val Ser Ile
 115 120 125

Pro His Gly Pro Asn Val Thr Val Arg Ala Asn Ile Ala Ala Ile Thr
 130 135 140

Glu Ser Asp Lys Phe Phe Ile Asn Gly Ser Asn Trp Glu Gly Ile Leu
 145 150 155 160

Gly Leu Ala Tyr Ala Glu Ile Ala Arg Pro Asp Asp Ser Leu Glu Pro
 165 170 175

Phe Phe Asp Ser Leu Val Lys Gln Thr His Val Pro Asn Leu Phe Ser
 180 185 190

Leu His Leu Cys Gly Ala Gly Phe Pro Leu Asn Gln Ser Glu Val Leu
 195 200 205

Ala Ser Val Gly Gly Ser Met Ile Ile Gly Gly Ile Asp His Ser Leu
 210 215 220

Tyr Thr Gly Ser Leu Trp Tyr Thr Pro Ile Arg Arg Glu Trp Tyr Tyr
 225 230 235 240

Glu Val Ile Ile Val Arg Val Glu Ile Asn Gly Gln Asp Leu Lys Met
 245 250 255

Asp Cys Lys Glu Tyr Asn Tyr Asp Lys Ser Ile Val Asp Ser Gly Thr
 260 265 270

Thr Asn Leu Arg Leu Pro Lys Lys Val Phe Glu Ala Ala Val Lys Ser
 275 280 285

Ile Lys Ala Ala Ser Ser Thr Glu Lys Phe Pro Asp Gly Phe Trp Leu
 290 295 300

Gly Glu Gln Leu Val Cys Trp Gln Ala Gly Thr Thr Pro Trp Asn Ile
 305 310 315 320

Phe Pro Val Ile Ser Leu Tyr Leu Met Gly Glu Val Thr Asn Gln Ser
 325 330 335

Phe Arg Ile Thr Ile Leu Pro Gln Gln Tyr Leu Arg Pro Val Glu Asp
 340 345 350
 Val Ala Thr Ser Gln Asp Asp Cys Tyr Lys Phe Ala Ile Ser Gln Ser
 355 360 365
 Ser Thr Gly Thr Val Met Gly Ala Val Ile Met Glu Gly Phe Tyr Val
 370 375 380
 Val Phe Asp Arg Ala Arg Lys Arg Ile Gly Phe Ala Val Ser Ala Cys
 385 390 395 400
 His Val His Asp Glu Phe Arg Thr Ala Ala Val Glu Gly Pro Phe Val
 405 410 415
 Thr Leu Asp Met Glu Asp Cys Gly Tyr Asn Ile Pro Gln Thr Asp Glu
 420 425 430

Ser

<210> 27
 <211> 1278
 <212> DNA
 <213> Homo sapiens

<400> 27
 atggctagca tgactggtgg acagcaaagt ggtcgcggat cgatgactat ctctgactct 60
 ccgctggact ctggtatcga aaccgacgga tcctttgtgg agatggtgga caacctgagg 120
 ggcaagtcgg ggcagggcta ctacgtggag atgaccgtgg gcagcccccc gcagacgctc 180
 aacatcctgg tggatacagg cagcagtaac ttgtcagtgg gtgctgcccc ccaccccttc 240
 ctgcatcgct actaccagag gcagctgtcc agcacatacc gggacctccg gaagggtgtg 300
 tatgtgccct acaccaggg caagtgggaa ggggagctgg gcaccgacct ggtaagcatc 360
 ccccatggcc ccaacgtcac tgtgcgtgcc aacattgctg ccatcactga atcagacaag 420
 ttcttcatca acggctccaa ctgggaaggc atcctggggc tggcctatgc tgagattgcc 480
 aggcctgacg actccctgga gcctttcttt gactctctgg taaagcagac ccacgttccc 540
 aacctcttct ccttgcacct ttgtggtgct ggcttcccc tcaaccagtc tgaagtgtg 600
 gcctctgtcg gagggagcat gatcattgga ggtatcgacc actcgtgtga cacaggcagt 660
 ctctggtata caccatccg gcgggagtgg tattatgagg tcatcattgt gcgggtggag 720
 atcaatggac aggatctgaa aatggactgc aaggagtaca actatgacaa gagcattgtg 780
 gacagtggca ccaccaacct tcgtttgccc aagaaagtgt ttgaagctgc agtcaaattc 840
 atcaaggcag cctcctccac ggagaagttc cctgatggtt tctggctagg agagcagctg 900

gtgtgctggc aagcaggcac cacccttgg aacattttcc cagtcacatctc actctaccta 960
atgggtgagg ttaccaacca gtccttccgc atcaccatcc ttccgcagca atacctgcgg 1020
ccagtgaag atgtggccac gtcccaagac gactgttaca agtttgccat ctcacagtca 1080
tccacgggca ctgttatggg agctgttatc atggagggct tctacgttgt ctttgatcgg 1140
gcccgaaaac gaattggctt tgctgtcagc gcttgccatg tgcaogatga gttcaggacg 1200
gcagcggtgg aaggcccttt tgtcaccttg gacatggaag actgtggcta caacattcca 1260
cagacagatg agtcatga 1278

<210> 28
<211> 425
<212> PRT
<213> Homo sapiens

<400> 28

Met Ala Ser Met Thr Gly Gly Gln Gln Met Gly Arg Gly Ser Met Thr
1 5 10 15

Ile Ser Asp Ser Pro Leu Asp Ser Gly Ile Glu Thr Asp Gly Ser Phe
20 25 30

Val Glu Met Val Asp Asn Leu Arg Gly Lys Ser Gly Gln Gly Tyr Tyr
35 40 45

Val Glu Met Thr Val Gly Ser Pro Pro Gln Thr Leu Asn Ile Leu Val
50 55 60

Asp Thr Gly Ser Ser Asn Phe Ala Val Gly Ala Ala Pro His Pro Phe
65 70 75 80

Leu His Arg Tyr Tyr Gln Arg Gln Leu Ser Ser Thr Tyr Arg Asp Leu
85 90 95

Arg Lys Gly Val Tyr Val Pro Tyr Thr Gln Gly Lys Trp Glu Gly Glu
100 105 110

Leu Gly Thr Asp Leu Val Ser Ile Pro His Gly Pro Asn Val Thr Val
115 120 125

Arg Ala Asn Ile Ala Ala Ile Thr Glu Ser Asp Lys Phe Phe Ile Asn
130 135 140

Gly Ser Asn Trp Glu Gly Ile Leu Gly Leu Ala Tyr Ala Glu Ile Ala
145 150 155 160

Arg Pro Asp Asp Ser Leu Glu Pro Phe Phe Asp Ser Leu Val Lys Gln
 165 170 175

Thr His Val Pro Asn Leu Phe Ser Leu His Leu Cys Gly Ala Gly Phe
 180 185 190

Pro Leu Asn Gln Ser Glu Val Leu Ala Ser Val Gly Gly Ser Met Ile
 195 200 205

Ile Gly Gly Ile Asp His Ser Leu Tyr Thr Gly Ser Leu Trp Tyr Thr
 210 215 220

Pro Ile Arg Arg Glu Trp Tyr Tyr Glu Val Ile Ile Val Arg Val Glu
 225 230 235 240

Ile Asn Gly Gln Asp Leu Lys Met Asp Cys Lys Glu Tyr Asn Tyr Asp
 245 250 255

Lys Ser Ile Val Asp Ser Gly Thr Thr Asn Leu Arg Leu Pro Lys Lys
 260 265 270

Val Phe Glu Ala Ala Val Lys Ser Ile Lys Ala Ala Ser Ser Thr Glu
 275 280 285

Lys Phe Pro Asp Gly Phe Trp Leu Gly Glu Gln Leu Val Cys Trp Gln
 290 295 300

Ala Gly Thr Thr Pro Trp Asn Ile Phe Pro Val Ile Ser Leu Tyr Leu
 305 310 315 320

Met Gly Glu Val Thr Asn Gln Ser Phe Arg Ile Thr Ile Leu Pro Gln
 325 330 335

Gln Tyr Leu Arg Pro Val Glu Asp Val Ala Thr Ser Gln Asp Asp Cys
 340 345 350

Tyr Lys Phe Ala Ile Ser Gln Ser Ser Thr Gly Thr Val Met Gly Ala
 355 360 365

Val Ile Met Glu Gly Phe Tyr Val Val Phe Asp Arg Ala Arg Lys Arg
 370 375 380

Ile Gly Phe Ala Val Ser Ala Cys His Val His Asp Glu Phe Arg Thr
 385 390 395 400

Ala Ala Val Glu Gly Pro Phe Val Thr Leu Asp Met Glu Asp Cys Gly
 405 410 415

Tyr Asn Ile Pro Gln Thr Asp Glu Ser
420 425

<210> 29
<211> 1362
<212> DNA
<213> Homo sapiens

<400> 29
atggcccaag ccctgccctg gctcctgctg tggatgggag cgggagtgct gcctgcccac 60
ggcaccacag acggcatccg gctgcccctg cgcagcggcc tggggggcgc cccctgggg 120
ctgcggctgc cccgggagac cgacgaagag cccgaggagc ccggccggag gggcagcttt 180
gtggagatgg tggacaacct gaggggcaag tgggggcagg gctactacgt ggagatgacc 240
gtgggcagcc ccccgagac gctcaacatc ctggtggata caggcagcag taactttgca 300
gtgggtgctg ccccccaccc ctctctgcat cgctactacc agaggcagct gtccagcaca 360
taccgggacc tccggaaggg tgtgtatgtg ccctacaccc agggcaagtg ggaaggggag 420
ctgggcaccg acctggtaag catcccccat ggccccaacg tcaactgtgc tgccaacatt 480
gctgccatca ctgaatcaga caagttcttc atcaacggct ccaactggga aggcattcctg 540
gggctggcct atgctgagat tgccaggcct gacgactccc tggagccttt ctttgactct 600
ctggtaaagc agaccacagt toccaacctc ttctccctgc acctttgtgg tgctggcttc 660
cccctcaacc agtctgaagt gctggcctct gtcggaggga gcatgacatc tggaggatc 720
gaccactcgc tgtacacagg cagtctctgg tatacaccca tccggcgagg gtggtattat 780
gaggtcatca ttgtgcgggt ggagatcaat ggacaggatc tgaaaatgga ctgcaaggag 840
tacaactatg acaagagcat tgtggacagt ggaccacca accttcgttt gccaagaaa 900
gtgtttgaag ctgcagtcaa atccatcaag gcagcctcct ccacggagaa gttccctgat 960
ggtttctggc taggagagca gctggtgtgc tggcaagcag gcaccacccc ttggaacatt 1020
ttcccagtca tctactcta cctaatgggt gaggttacca accagtcctt ccgcatcacc 1080
atccttccgc agcaatacct gcggccagtg gaagatgtgg ccacgtccca agacgactgt 1140
tacaagtttg ccatctcaca gtcattccac ggcactgtta tgggagctgt tatcatggag 1200
ggcttctacg ttgtctttga tggggcccga aaacgaattg gctttgctgt cagcgcttgc 1260
catgtgcacg atgagttcag gacggcagcg gtggaaggcc cttttgtcac cttggacatg 1320
gaagactgtg gctacaacat tccacagaca gatgagtcac ga 1362

<210> 30
<211> 453
<212> PRT
<213> Homo sapiens

<400> 30

Met Ala Gln Ala Leu Pro Trp Leu Leu Leu Trp Met Gly Ala Gly Val
1 5 10 15

Leu Pro Ala His Gly Thr Gln His Gly Ile Arg Leu Pro Leu Arg Ser
20 25 30

Gly Leu Gly Gly Ala Pro Leu Gly Leu Arg Leu Pro Arg Glu Thr Asp
35 40 45

Glu Glu Pro Glu Glu Pro Gly Arg Arg Gly Ser Phe Val Glu Met Val
50 55 60

Asp Asn Leu Arg Gly Lys Ser Gly Gln Gly Tyr Tyr Val Glu Met Thr
65 70 75 80

Val Gly Ser Pro Pro Gln Thr Leu Asn Ile Leu Val Asp Thr Gly Ser
85 90 95

Ser Asn Phe Ala Val Gly Ala Ala Pro His Pro Phe Leu His Arg Tyr
100 105 110

Tyr Gln Arg Gln Leu Ser Ser Thr Tyr Arg Asp Leu Arg Lys Gly Val
115 120 125

Tyr Val Pro Tyr Thr Gln Gly Lys Trp Glu Gly Glu Leu Gly Thr Asp
130 135 140

Leu Val Ser Ile Pro His Gly Pro Asn Val Thr Val Arg Ala Asn Ile
145 150 155 160

Ala Ala Ile Thr Glu Ser Asp Lys Phe Phe Ile Asn Gly Ser Asn Trp
165 170 175

Glu Gly Ile Leu Gly Leu Ala Tyr Ala Glu Ile Ala Arg Pro Asp Asp
180 185 190

Ser Leu Glu Pro Phe Phe Asp Ser Leu Val Lys Gln Thr His Val Pro
195 200 205

Asn Leu Phe Ser Leu Gln Leu Cys Gly Ala Gly Phe Pro Leu Asn Gln
210 215 220

Ser Glu Val Leu Ala Ser Val Gly Gly Ser Met Ile Ile Gly Gly Ile
225 230 235 240

Asp His Ser Leu Tyr Thr Gly Ser Leu Trp Tyr Thr Pro Ile Arg Arg
 245 250 255
 Glu Trp Tyr Tyr Glu Val Ile Ile Val Arg Val Glu Ile Asn Gly Gln
 260 265 270
 Asp Leu Lys Met Asp Cys Lys Glu Tyr Asn Tyr Asp Lys Ser Ile Val
 275 280 285
 Asp Ser Gly Thr Thr Asn Leu Arg Leu Pro Lys Lys Val Phe Glu Ala
 290 295 300
 Ala Val Lys Ser Ile Lys Ala Ala Ser Ser Thr Glu Lys Phe Pro Asp
 305 310 315 320
 Gly Phe Trp Leu Gly Glu Gln Leu Val Cys Trp Gln Ala Gly Thr Thr
 325 330 335
 Pro Trp Asn Ile Phe Pro Val Ile Ser Leu Tyr Leu Met Gly Glu Val
 340 345 350
 Thr Asn Gln Ser Phe Arg Ile Thr Ile Leu Pro Gln Gln Tyr Leu Arg
 355 360 365
 Pro Val Glu Asp Val Ala Thr Ser Gln Asp Asp Cys Tyr Lys Phe Ala
 370 375 380
 Ile Ser Gln Ser Ser Thr Gly Thr Val Met Gly Ala Val Ile Met Glu
 385 390 395 400
 Gly Phe Tyr Val Val Phe Asp Arg Ala Arg Lys Arg Ile Gly Phe Ala
 405 410 415
 Val Ser Ala Cys His Val His Asp Glu Phe Arg Thr Ala Ala Val Glu
 420 425 430
 Gly Pro Phe Val Thr Leu Asp Met Glu Asp Cys Gly Tyr Asn Ile Pro
 435 440 445
 Gln Thr Asp Glu Ser
 450

<210> 31
 <211> 1380
 <212> DNA
 <213> Homo sapiens

<400> 31
atggcccaag ccttgccctg gctcctgctg tggatgggcg cgggagtgt gctgcccac 60
ggcaccacagc acggcatccg gctgcccctg cgcagcggcc tggggggcg ccccttggg 120
ctgcgggtgc cccgggagac cgacgaagag cccgaggagc ccggccggag gggcagcttt 180
gtggagatgg tggacaacct gaggggcaag tcggggcagg gctactacgt ggagatgacc 240
gtgggcagcc ccccgagac gctcaacatc ctggtggata caggcagcag taactttgca 300
gtgggtgctg ccccccaccc ctctctgcat cgctactacc agaggcagct gtccagcaca 360
taccgggacc tccggaaggg tgtgtatgtg ccctacaccc agggcaagt ggaaggggag 420
ctgggcaccg acctggtgtaag catcccccat ggccccaacg tctactgtgcg tgccaacatt 480
gctgccatca ctgaatcaga caagttcttc atcaacggct ccaactggga aggcattcctg 540
gggctggcct atgtgagat tgccaggcct gacgactccc tggagccttt ctttgactct 600
ctggtaaagc agaccacgt tcccaacctc ttctccctgc acctttgtgg tcttggttc 660
ccctcaacc agtctgaagt gctggcctct gtcggaggga gcatgatcat tggaggtatc 720
gaccactcgc tgtacacagg cagtctctgg tatacaccca tccggcggga gtggtattat 780
gaggtcatca ttgtgctggg ggagatcaat ggacaggatc tgaaaatgga ctgcaaggag 840
tacaactatg acaagagcat tgtggacagt ggcaccacca accttcgttt gcccaagaaa 900
gtgtttgaag ctgcagtcaa atccatcaag gcagcctcct ccacggagaa gttccctgat 960
ggtttctggc taggagagca gctggtgtgc tggcaagcag gcaccacccc ttggaacatt 1020
ttcccagtc tctcactcta cctaattgggt gaggttacca accagtctct ccgcattcacc 1080
atccttcgc agcaatacct gcggccagtg gaagatgtgg ccacgtccca agacgactgt 1140
tacaagtttg ccatctcaca gtcattccag ggcactgtta tgggagctgt tatcatggag 1200
ggcttctacg ttgtctttga tcggggcccga aaacgaattg gctttgctgt cagcgcttgc 1260
catgtgcacg atgagttcag gacggcagcg gtggaaggcc cttttgtcac cttggacatg 1320
gaagactgtg gctacaacat tccacagaca gatgagtcac agcagcagca gcagcagtga 1380

<210> 32
<211> 459
<212> PRT
<213> Homo sapiens

<400> 32

Met Ala Gln Ala Leu Pro Trp Leu Leu Leu Trp Met Gly Ala Gly Val
1 5 10 15

Leu Pro Ala His Gly Thr Gln His Gly Ile Arg Leu Pro Leu Arg Ser
20 25 30

Gly Leu Gly Gly Ala Pro Leu Gly Leu Arg Leu Pro Arg Glu Thr Asp
 35 40 45
 Glu Glu Pro Glu Glu Pro Gly Arg Arg Gly Ser Phe Val Glu Met Val
 50 55 60
 Asp Asn Leu Arg Gly Lys Ser Gly Gln Gly Tyr Tyr Val Glu Met Thr
 65 70 75 80
 Val Gly Ser Pro Pro Gln Thr Leu Asn Ile Leu Val Asp Thr Gly Ser
 85 90 95
 Ser Asn Phe Ala Val Gly Ala Ala Pro His Pro Phe Leu His Arg Tyr
 100 105 110
 Tyr Gln Arg Gln Leu Ser Ser Thr Tyr Arg Asp Leu Arg Lys Gly Val
 115 120 125
 Tyr Val Pro Tyr Thr Gln Gly Lys Trp Glu Gly Glu Leu Gly Thr Asp
 130 135 140
 Leu Val Ser Ile Pro His Gly Pro Asn Val Thr Val Arg Ala Asn Ile
 145 150 155 160
 Ala Ala Ile Thr Glu Ser Asp Lys Phe Phe Ile Asn Gly Ser Asn Trp
 165 170 175
 Glu Gly Ile Leu Gly Leu Ala Tyr Ala Glu Ile Ala Arg Pro Asp Asp
 180 185 190
 Ser Leu Glu Pro Phe Phe Asp Ser Leu Val Lys Gln Thr His Val Pro
 195 200 205
 Asn Leu Phe Ser Leu Gln Leu Cys Gly Ala Gly Phe Pro Leu Asn Gln
 210 215 220
 Ser Glu Val Leu Ala Ser Val Gly Gly Ser Met Ile Ile Gly Gly Ile
 225 230 235 240
 Asp His Ser Leu Tyr Thr Gly Ser Leu Trp Tyr Thr Pro Ile Arg Arg
 245 250 255
 Glu Trp Tyr Tyr Glu Val Ile Ile Val Arg Val Glu Ile Asn Gly Gln
 260 265 270
 Asp Leu Lys Met Asp Cys Lys Glu Tyr Asn Tyr Asp Lys Ser Ile Val
 275 280 285

Asp Ser Gly Thr Thr Asn Leu Arg Leu Pro Lys Lys Val Phe Glu Ala
290 295 300

Ala Val Lys Ser Ile Lys Ala Ala Ser Ser Thr Glu Lys Phe Pro Asp
305 310 315 320

Gly Phe Trp Leu Gly Glu Gln Leu Val Cys Trp Gln Ala Gly Thr Thr
325 330 335

Pro Trp Asn Ile Phe Pro Val Ile Ser Leu Tyr Leu Met Gly Glu Val
340 345 350

Thr Asn Gln Ser Phe Arg Ile Thr Ile Leu Pro Gln Gln Tyr Leu Arg
355 360 365

Pro Val Glu Asp Val Ala Thr Ser Gln Asp Asp Cys Tyr Lys Phe Ala
370 375 380

Ile Ser Gln Ser Ser Thr Gly Thr Val Met Gly Ala Val Ile Met Glu
385 390 395 400

Gly Phe Tyr Val Val Phe Asp Arg Ala Arg Lys Arg Ile Gly Phe Ala
405 410 415

Val Ser Ala Cys His Val His Asp Glu Phe Arg Thr Ala Ala Val Glu
420 425 430

Gly Pro Phe Val Thr Leu Asp Met Glu Asp Cys Gly Tyr Asn Ile Pro
435 440 445

Gln Thr Asp Glu Ser His His His His His His
450 455

<210> 33
<211> 25
<212> PRT
<213> Homo sapiens

<400> 33

Ser Glu Gln Gln Arg Arg Pro Arg Asp Pro Glu Val Val Asn Asp Glu
1 5 10 15

Ser Ser Leu Val Arg His Arg Trp Lys
20 25

<210> 34
<211> 19
<212> PRT
<213> Homo sapiens

<400> 34

Ser Glu Gln Leu Arg Gln Gln His Asp Asp Phe Ala Asp Asp Ile Ser
1 5 10 15

Leu Leu Lys

<210> 35

<211> 29

<212> DNA

<213> Homo sapiens

<400> 35

gtggatccac ccagcacggc atccggctg

29

<210> 36

<211> 36

<212> DNA

<213> Homo sapiens

<400> 36

gaaagctttc atgactcatc tgtctgtgga atgttg

36

<210> 37

<211> 39

<212> DNA

<213> Homo sapiens

<400> 37

gatcgatgac tatctctgac tctccgctg aacaggacg

39

<210> 38

<211> 39

<212> DNA

<213> Homo sapiens

<400> 38

gatccgtcct gttcacgcgg agagtcagag atagtcac

39

<210> 39

<211> 77

<212> DNA

<213> Artificial Sequence

<220>

<223> Hu-Asp2

<400> 39

cggcatccgg ctgccctgc gtagcggctt gggtaggtgct ccaactgggtc tgcgtctgcc

60

ccgggagacc gacgaag

77

<210> 40
 <211> 77
 <212> DNA
 <213> Artificial sequence

 <220>
 <223> Hu-Asp2

 <400> 40
 cttcgtcggg ctcccggggc agacgcagac ccagtggagc accacccaga ccgctacgca 60
 ggggcagccg gatgccg 77

 <210> 41
 <211> 51
 <212> DNA
 <213> Artificial sequence

 <220>
 <223> Caspase-8 Cleavage Site

 <400> 41
 gatcgatgac tatctctgac tctccgctgg actctggtat cgaaaccgac g 51

 <210> 42
 <211> 51
 <212> DNA
 <213> Artificial sequence

 <220>
 <223> Caspase-8 Cleavage Site

 <400> 42
 gatccgtcgg ttccgatacc agagtccagc ggagagtcag agatagtcac c 51

 <210> 43
 <211> 32
 <212> DNA
 <213> Homo sapiens

 <400> 43
 aaggatcctt tgtggagatg gtggacaacc tg 32

 <210> 44
 <211> 36
 <212> DNA
 <213> Homo sapiens

 <400> 44
 gaaagctttc atgactcacc tgtctgtgga atgttg 36

 <210> 45
 <211> 24
 <212> DNA
 <213> Artificial sequence

<220>
 <223> 6-His tag

 <400> 45
 gatcgcacatca tcaccatcac catg 24

 <210> 46
 <211> 24
 <212> DNA
 <213> Artificial sequence

 <220>
 <223> 6-His tag

 <400> 46
 gatccatggt gatggtgatg atgc 24

 <210> 47
 <211> 22
 <212> DNA
 <213> Artificial sequence

 <220>
 <223> Primer

 <400> 47
 gactgaccac tcgaccaggt tc 22

 <210> 48
 <211> 51
 <212> DNA
 <213> Artificial sequence

 <220>
 <223> Primer

 <400> 48
 cgaattaaat tccagcacac tggctacttc ttgttctgca tctcaaagaa c 51

 <210> 49
 <211> 26
 <212> DNA
 <213> Artificial sequence

 <220>
 <223> Primer

 <400> 49
 cgaattaaat tccagcacac tggcta 26

 <210> 50
 <211> 1287
 <212> DNA
 <213> Artificial sequence

 <220>
 <223> Hu-Asp2(b) delta TM

<400> 50
atggcccaag ccctgccctg gctcctgctg tggatgggcg cgggagtgt gcttgcacac 60
ggcaccacagc acggcatccg gctgcccctg cgcagcggcc tgggggggccc ccccttggg 120
ctgcggctgc cccgggagac cgacgaagag cccgaggagc ccggccggag gggcagcttt 180
gtggagatgg tggacaacct gaggggcaag tcggggcagg gctactacgt ggagatgacc 240
gtgggcagcc ccccgagac gctcaacatc ctggtggata caggcagcag taactttgca 300
gtgggtgctg cccccaccc cttcctgcat cgctactacc agaggcagct gtccagcaca 360
taccgggacc tccggaagg tgtgtatgtg ccctacacc agggcaagt ggaaggggag 420
ctgggcaccg acctggttaag catcccccat ggccccaacg tcaactgtgcg tgccaacatt 480
gctgccatca ctgaatcaga caagttcttc atcaacggct ccaactggga aggcattcctg 540
gggctggcct atgctgagat tgccaggctt tgtggtgctg gcttccccct caaccagtct 600
gaagtgtggt cctctgtcgg agggagcatg atcattggag gtatcgacca ctgcgtgtac 660
acaggcagtc tctggtatac acccatccgg cgggagtggg attatgaggt catcattgtg 720
cgggtggaga tcaatggaca ggatctgaaa atggactgca aggagtacaa ctatgacaag 780
agcattgtgg acagtggcac caccaacctt cgtttgccca agaaagtgtt tgaagctgca 840
gtcaaatcca tcaaggcagc ctctccacg gagaagttcc ctgatggttt ctggctagga 900
gagcagctgg tgtgctggca agcaggcacc accccttggg acattttccc agtcatctca 960
ctctacctaa tgggtgaggt taccaaccag tccttcgca tcaccatcct tccgcagcaa 1020
tacctgcggc cagtgaaga tgtggccacg tccaagacg actgttataa gtttgccatc 1080
tcacagtcac ccacgggac tggtatggga gctgttatca tggagggctt ctacgttgtc 1140
tttgatcggg cccgaaaacg aattggcttt gctgtcagcg cttgccatgt gcacgatgag 1200
ttcaggacgg cagcgggtgga aggcctttt gtcaccttg acatggaaga ctgtggctac 1260
aacattccac agacagatga gtcatga 1287

<210> 51
<211> 428
<212> PRT
<213> Artificial sequence

<220>
<223> Hu-Asp2(b) delta TM

<400> 51

Met Ala Gln Ala Leu Pro Trp Leu Leu Leu Trp Met Gly Ala Gly Val
1 5 10 15

Leu Pro Ala His Gly Thr Gln His Gly Ile Arg Leu Pro Leu Arg Ser
20 25 30

Gly Leu Gly Gly Ala Pro Leu Gly Leu Arg Leu Pro Arg Glu Thr Asp
 35 40 45
 Glu Glu Pro Glu Glu Pro Gly Arg Arg Gly Ser Phe Val Glu Met Val
 50 55 60
 Asp Asn Leu Arg Gly Lys Ser Gly Gln Gly Tyr Tyr Val Glu Met Thr
 65 70 75 80
 Val Gly Ser Pro Pro Gln Thr Leu Asn Ile Leu Val Asp Thr Gly Ser
 85 90 95
 Ser Asn Phe Ala Val Gly Ala Ala Pro His Pro Phe Leu His Arg Tyr
 100 105 110
 Tyr Gln Arg Gln Leu Ser Ser Thr Tyr Arg Asp Leu Arg Lys Gly Val
 115 120 125
 Tyr Val Pro Tyr Thr Gln Gly Lys Trp Glu Gly Glu Leu Gly Thr Asp
 130 135 140
 Leu Val Ser Ile Pro His Gly Pro Asn Val Thr Val Arg Ala Asn Ile
 145 150 155 160
 Ala Ala Ile Thr Glu Ser Asp Lys Phe Phe Ile Asn Gly Ser Asn Trp
 165 170 175
 Glu Gly Ile Leu Gly Leu Ala Tyr Ala Glu Ile Ala Arg Leu Cys Gly
 180 185 190
 Ala Gly Phe Pro Leu Asn Gln Ser Glu Val Leu Ala Ser Val Gly Gly
 195 200 205
 Ser Met Ile Ile Gly Gly Ile Asp His Ser Leu Tyr Thr Gly Ser Leu
 210 215 220
 Trp Tyr Thr Pro Ile Arg Arg Glu Trp Tyr Tyr Glu Val Ile Ile Val
 225 230 235 240
 Arg Val Glu Ile Asn Gly Gln Asp Leu Lys Met Asp Cys Lys Glu Tyr
 245 250 255
 Asn Tyr Asp Lys Ser Ile Val Asp Ser Gly Thr Thr Asn Leu Arg Leu
 260 265 270
 Pro Lys Lys Val Phe Glu Ala Ala Val Lys Ser Ile Lys Ala Ala Ser
 275 280 285

Ser Thr Glu Lys Phe Pro Asp Gly Phe Trp Leu Gly Glu Gln Leu Val
 290 295 300
 Cys Trp Gln Ala Gly Thr Thr Pro Trp Asn Ile Phe Pro Val Ile Ser
 305 310 315 320
 Leu Tyr Leu Met Gly Glu Val Thr Asn Gln Ser Phe Arg Ile Thr Ile
 325 330 335
 Leu Pro Gln Gln Tyr Leu Arg Pro Val Glu Asp Val Ala Thr Ser Gln
 340 345 350
 Asp Asp Cys Tyr Lys Phe Ala Ile Ser Gln Ser Ser Thr Gly Thr Val
 355 360 365
 Met Gly Ala Val Ile Met Glu Gly Phe Tyr Val Val Phe Asp Arg Ala
 370 375 380
 Arg Lys Arg Ile Gly Phe Ala Val Ser Ala Cys His Val His Asp Glu
 385 390 395 400
 Phe Arg Thr Ala Ala Val Glu Gly Pro Phe Val Thr Leu Asp Met Glu
 405 410 415
 Asp Cys Gly Tyr Asn Ile Pro Gln Thr Asp Glu Ser
 420 425

<210> 52
 <211> 1305
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Hu-Asp2(b) delta TM

<400> 52
 atggcccaag ccctgccctg gctcctgctg tggatgggag cgggagtgtt gctgcccac 60
 ggcacccagc acggcatccg gctgcccctg cgcagcggcc tgggggggag ccccctgggg 120
 ctgctggctgc cccgggagac cgacgaagag cccgaggagc ccggccggag gggcagcttt 180
 gtggagatgg tggacaacct gaggggcaag tcggggcagg gctactacgt ggagatgacc 240
 gtgggcagcc ccccgagac gctcaacatc ctggtggata caggcagcag taactttgca 300
 gtgggtgctg cccccaccc ctctctgcat cgctactacc agaggcagct gtccagcaca 360
 taccgggacc tccggaaggg tgtgtatgtg ccctacaccc agggcaagtg ggaaggggag 420
 ctgggcaccg acctggtgtaag catcccccat ggccccaacg tcaactgtgc tgccaacatt 480
 gctgcatca ctgaatcaga caagttcttc atcaacggct ccaactggga aggcacacct 540

gggctggcct atgctgagat tgccaggctt tgtggtgctg gcttccccct caaccagtct 600
 gaagtgtggt cctctgtcgg agggagcatg atcattggag gtatcgacca ctgctgtac 660
 acaggcagtc tctggtatac acccatccgg cgggagtggt attatgaggt catcattgtg 720
 cgggtggaga tcaatggaca ggatctgaaa atggactgca aggagtacaa ctatgacaag 780
 agcattgtgg acagtggcac caccaacctt cgtttgccca agaaagtgtt tgaagctgca 840
 gtcaaatacca tcaaggcagc ctctccacg gagaagttcc ctgatggttt ctggctagga 900
 gagcagctgg tgtgctggca agcaggcacc accccttgga acattttccc agtcatctca 960
 ctctacctaa tgggtgaggt taccaaccag tccttcgcga tcaccatcct tccgcagcaa 1020
 tacctgcggc cagtgaaga tgtggccacg tccaagacg actgttataa gtttgccatc 1080
 tcacagtcac ccacgggcac tggtatggga gctgttatca tggagggctt ctacgttgtc 1140
 tttgatcggg cccgaaaacg aattggcttt gctgtcagcg cttgccatgt gcacgatgag 1200
 ttcaggacgg cagcgggtgga aggccctttt gtcaccttgg acatggaaga ctgtggctac 1260
 aacattccac agacagatga gtcacagcag cagcagcagc agtga 1305

<210> 53
 <211> 434
 <212> PRT
 <213> Artificial sequence

<220>
 <223> Hu-Asp2(b) delta TM

<400> 53

Met Ala Gln Ala Leu Pro Trp Leu Leu Leu Trp Met Gly Ala Gly Val
 1 5 10 15

Leu Pro Ala His Gly Thr Gln His Gly Ile Arg Leu Pro Leu Arg Ser
 20 25 30

Gly Leu Gly Gly Ala Pro Leu Gly Leu Arg Leu Pro Arg Glu Thr Asp
 35 40 45

Glu Glu Pro Glu Glu Pro Gly Arg Arg Gly Ser Phe Val Glu Met Val
 50 55 60

Asp Asn Leu Arg Gly Lys Ser Gly Gln Gly Tyr Tyr Val Glu Met Thr
 65 70 75 80

Val Gly Ser Pro Pro Gln Thr Leu Asn Ile Leu Val Asp Thr Gly Ser
 85 90 95

Ser Asn Phe Ala Val Gly Ala Ala Pro His Pro Phe Leu His Arg Tyr
 100 105 110

Tyr Gln Arg Gln Leu Ser Ser Thr Tyr Arg Asp Leu Arg Lys Gly Val
 115 120 125

Tyr Val Pro Tyr Thr Gln Gly Lys Trp Glu Gly Glu Leu Gly Thr Asp
 130 135 140

Leu Val Ser Ile Pro His Gly Pro Asn Val Thr Val Arg Ala Asn Ile
 145 150 155 160

Ala Ala Ile Thr Glu Ser Asp Lys Phe Phe Ile Asn Gly Ser Asn Trp
 165 170 175

Glu Gly Ile Leu Gly Leu Ala Tyr Ala Glu Ile Ala Arg Leu Cys Gly
 180 185 190

Ala Gly Phe Pro Leu Asn Gln Ser Glu Val Leu Ala Ser Val Gly Gly
 195 200 205

Ser Met Ile Ile Gly Gly Ile Asp His Ser Leu Tyr Thr Gly Ser Leu
 210 215 220

Trp Tyr Thr Pro Ile Arg Arg Glu Trp Tyr Tyr Glu Val Ile Ile Val
 225 230 235 240

Arg Val Glu Ile Asn Gly Gln Asp Leu Lys Met Asp Cys Lys Glu Tyr
 245 250 255

Asn Tyr Asp Lys Ser Ile Val Asp Ser Gly Thr Thr Asn Leu Arg Leu
 260 265 270

Pro Lys Lys Val Phe Glu Ala Ala Val Lys Ser Ile Lys Ala Ala Ser
 275 280 285

Ser Thr Glu Lys Phe Pro Asp Gly Phe Trp Leu Gly Glu Gln Leu Val
 290 295 300

Cys Trp Gln Ala Gly Thr Thr Pro Trp Asn Ile Phe Pro Val Ile Ser
 305 310 315 320

Leu Tyr Leu Met Gly Glu Val Thr Asn Gln Ser Phe Arg Ile Thr Ile
 325 330 335

Leu Pro Gln Gln Tyr Leu Arg Pro Val Glu Asp Val Ala Thr Ser Gln
 340 345 350

Asp Asp Cys Tyr Lys Phe Ala Ile Ser Gln Ser Ser Thr Gly Thr Val
 355 360 365

Met Gly Ala Val Ile Met Glu Gly Phe Tyr Val Val Phe Asp Arg Ala
 370 375 380

Arg Lys Arg Ile Gly Phe Ala Val Ser Ala Cys His Val His Asp Glu
 385 390 395 400

Phe Arg Thr Ala Ala Val Glu Gly Pro Phe Val Thr Leu Asp Met Glu
 405 410 415

Asp Cys Gly Tyr Asn Ile Pro Gln Thr Asp Glu Ser His His His His
 420 425 430

His His

<210> 54
 <211> 2310
 <212> DNA
 <213> Homo sapiens

<400> 54
 atgctgcccc gtttggaact gtcctgctg gccgcctgga cggtcgggc gctggaggta 60
 cccactgatg gtaatgctgg cctgctggct gaaccccaga ttgccatgtt ctgtggcaga 120
 ctgaacatgc acatgaatgt ccagaatggg aagtgggatt cagatccatc agggacaaaa 180
 acctgcattg ataccaagga aggcacacct cagtattgcc aagaagtcta ccctgaactg 240
 cagatcacca atgtggtaga agccaaccac ccagtgaacca tccagaactg gtgcaagcgg 300
 ggccgcaagc agtgcaagac ccacccccac tttgtgattc cctaccgctg cttagtgtgt 360
 gagtttgtaa gtgatgcct tctcgcttcc gacaagtga aattcttaca ccaggagagg 420
 atggatgttt gcgaaactca tcttccactg cacaccgtcg ccaaagagac atgcagtgag 480
 aagagtacca acttgcatga ctacggcatg ttgctgcct gcggaattga caagttccga 540
 ggggtagagt ttgtgtgttg cccactggct gaagaaagtg acaatgtgga ttctgctgat 600
 gcggaggagg atgactcgga tgtctggtgg ggccgagcag acacagacta tgcagatggg 660
 agtgaagaca aagtagtaga agtagcagag gaggaagaag tggctgaggt ggaagaagaa 720
 gaagccgatg atgacgagga cgatgaggat ggtgatgagg tagaggaaga ggctgaggaa 780
 ccctacgaag aagccacaga gagaaccacc agcattgcca ccaccaccac caccaccaca 840
 gagtctgtgg aagaggtggt tcgagaggtg tgctctgaac aagccgagac ggggccgtgc 900
 cgagcaatga tctcccgtg gtactttgat gtgactgaag ggaagtgtgc ccatttcttt 960
 tacggcggat gtggcggcaa ccggaacaac ttgacacag aagagtactg catggccgtg 1020
 tgtggcagcg ccattgtcca aagtttactc aagactaccc aggaacctct tggccgagat 1080

cctgttaaac	ttcctacaac	agcagccagt	accctgatg	ccgttgacaa	gtatctcgag	1140
acacctgggg	atgagaatga	acatgccc	atccagaaag	caaagagag	gcttgaggcc	1200
aagcaccgag	agagaatgtc	ccaggtc	atgagaatggg	aagaggcaga	acgtcaagca	1260
aagaacttgc	ctaaagctga	taagaaggca	gttatccagc	atttccagga	gaaagtggaa	1320
tctttggaac	aggaagcagc	caacgagaga	cagcagctgg	tggagacaca	catggccaga	1380
gtggaagcca	tgctcaatga	ccgccgccgc	ctggccctgg	agaactacat	caccgctctg	1440
caggctgttc	ctcctcggcc	tcgtcacgtg	ttcaatatgc	taaagaagta	tgtccgcgca	1500
gaacagaagg	acagacagca	cacctaaag	catttcgagc	atgtgcgc	ggtggatccc	1560
aagaaagccg	ctcagatccg	gtcccagggt	atgacacacc	tccgtgtgat	ttatgagcgc	1620
atgaatcagt	ctctctccct	gctctacaac	gtgcctgcag	tggccgagga	gattcaggat	1680
gaagttgatg	agctgcttca	gaaagagcaa	aactattcag	atgacgtctt	ggccaacatg	1740
attagtgaac	caaggatcag	ttacggaaac	gatgctctca	tgccatcttt	gaccgaaacg	1800
aaaaccaccg	tggagctcct	tcccgtgaat	ggagagttca	gcctggacga	tctccagccg	1860
tggcattctt	ttggggctga	ctctgtgcca	gccaacacag	aaaacgaagt	tgagcctgtt	1920
gatgcccgcc	ctyctgccga	ccgaggactg	accactcgac	caggttctgg	gttgacaaat	1980
atcaagacgg	aggagatctc	tgaagtgaag	atggatgcag	aattccgaca	tgactcagga	2040
tatgaagttc	atcatcaaaa	attggtgttc	tttgcagaag	atgtgggttc	aaacaaaggt	2100
gcaatcattg	gactcatggt	gggcggtgtt	gtcatagcga	cagtgatcgt	catcaccttg	2160
gtgatgctga	agaagaaaca	gtacacatcc	attcatcatg	gtgtggtgga	ggttgacgcc	2220
gctgtcacc	cagaggagcg	ccacctgtcc	aagatgcagc	agaacggcta	cgaaaatcca	2280
acctacaagt	tctttgagca	gatgcagaac				2310

<210> 55
 <211> 770
 <212> PRT
 <213> Homo sapiens

<400> 55

Met	Leu	Pro	Gly	Leu	Ala	Leu	Leu	Leu	Leu	Ala	Ala	Trp	Thr	Ala	Arg
1				5					10					15	

Ala	Leu	Glu	Val	Pro	Thr	Asp	Gly	Asn	Ala	Gly	Leu	Leu	Ala	Glu	Pro
			20					25					30		

Gln	Ile	Ala	Met	Phe	Cys	Gly	Arg	Leu	Asn	Met	His	Met	Asn	Val	Gln
		35					40				45				

Asn Gly Lys Trp Asp Ser Asp Pro Ser Gly Thr Lys Thr Cys Ile Asp
 50 55 60

Thr Lys Glu Gly Ile Leu Gln Tyr Cys Gln Glu Val Tyr Pro Glu Leu
 65 70 75 80

Gln Ile Thr Asn Val Val Glu Ala Asn Gln Pro Val Thr Ile Gln Asn
 85 90 95

Trp Cys Lys Arg Gly Arg Lys Gln Cys Lys Thr His Pro His Phe Val
 100 105 110

Ile Pro Tyr Arg Cys Leu Val Gly Glu Phe Val Ser Asp Ala Leu Leu
 115 120 125

Val Pro Asp Lys Cys Lys Phe Leu His Gln Glu Arg Met Asp Val Cys
 130 135 140

Glu Thr His Leu His Trp His Thr Val Ala Lys Glu Thr Cys Ser Glu
 145 150 155 160

Lys Ser Thr Asn Leu His Asp Tyr Gly Met Leu Leu Pro Cys Gly Ile
 165 170 175

Asp Lys Phe Arg Gly Val Glu Phe Val Cys Cys Pro Leu Ala Glu Glu
 180 185 190

Ser Asp Asn Val Asp Ser Ala Asp Ala Glu Glu Asp Asp Ser Asp Val
 195 200 205

Trp Trp Gly Gly Ala Asp Thr Asp Tyr Ala Asp Gly Ser Glu Asp Lys
 210 215 220

Val Val Glu Val Ala Glu Glu Glu Glu Val Ala Glu Val Glu Glu Glu
 225 230 235 240

Glu Ala Asp Asp Asp Glu Asp Asp Glu Asp Gly Asp Glu Val Glu Glu
 245 250 255

Glu Ala Glu Glu Pro Tyr Glu Glu Ala Thr Glu Arg Thr Thr Ser Ile
 260 265 270

Ala Thr Thr Thr Thr Thr Thr Thr Glu Ser Val Glu Glu Val Val Arg
 275 280 285

Glu Val Cys Ser Glu Gln Ala Glu Thr Gly Pro Cys Arg Ala Met Ile
 290 295 300

Ser Arg Trp Tyr Phe Asp Val Thr Glu Gly Lys Cys Ala Pro Phe Phe
 305 310 315 320
 Tyr Gly Gly Cys Gly Gly Asn Arg Asn Asn Phe Asp Thr Glu Glu Tyr
 325 330 335
 Cys Met Ala Val Cys Gly Ser Ala Met Ser Gln Ser Leu Leu Lys Thr
 340 345 350
 Thr Gln Glu Pro Leu Ala Arg Asp Pro Val Lys Leu Pro Thr Thr Ala
 355 360 365
 Ala Ser Thr Pro Asp Ala Val Asp Lys Tyr Leu Glu Thr Pro Gly Asp
 370 375 380
 Glu Asn Glu His Ala His Phe Gln Lys Ala Lys Glu Arg Leu Glu Ala
 385 390 395 400
 Lys His Arg Glu Arg Met Ser Gln Val Met Arg Glu Trp Glu Glu Ala
 405 410 415
 Glu Arg Gln Ala Lys Asn Leu Pro Lys Ala Asp Lys Lys Ala Val Ile
 420 425 430
 Gln His Phe Gln Glu Lys Val Glu Ser Leu Glu Gln Glu Ala Ala Asn
 435 440 445
 Glu Arg Gln Gln Leu Val Glu Thr His Met Ala Arg Val Glu Ala Met
 450 455 460
 Leu Asn Asp Arg Arg Arg Leu Ala Leu Glu Asn Tyr Ile Thr Ala Leu
 465 470 475 480
 Gln Ala Val Pro Pro Arg Pro Arg His Val Phe Asn Met Leu Lys Lys
 485 490 495
 Tyr Val Arg Ala Glu Gln Lys Asp Arg Gln His Thr Leu Lys His Phe
 500 505 510
 Glu His Val Arg Met Val Asp Pro Lys Lys Ala Ala Gln Ile Arg Ser
 515 520 525
 Gln Val Met Thr His Leu Arg Val Ile Tyr Glu Arg Met Asn Gln Ser
 530 535 540
 Leu Ser Leu Leu Tyr Asn Val Pro Ala Val Ala Glu Glu Ile Gln Asp
 545 550 555 560

Glu Val Asp Glu Leu Leu Gln Lys Glu Gln Asn Tyr Ser Asp Asp Val
565 570 575

Leu Ala Asn Met Ile Ser Glu Pro Arg Ile Ser Tyr Gly Asn Asp Ala
580 585 590

Leu Met Pro Ser Leu Thr Glu Thr Lys Thr Thr Val Glu Leu Leu Pro
595 600 605

Val Asn Gly Glu Phe Ser Leu Asp Asp Leu Gln Pro Trp His Ser Phe
610 615 620

Gly Ala Asp Ser Val Pro Ala Asn Thr Glu Asn Glu Val Glu Pro Val
625 630 635 640

Asp Ala Arg Pro Ala Ala Asp Arg Gly Leu Thr Thr Arg Pro Gly Ser
645 650 655

Gly Leu Thr Asn Ile Lys Thr Glu Glu Ile Ser Glu Val Lys Met Asp
660 665 670

Ala Glu Phe Arg His Asp Ser Gly Tyr Glu Val His His Gln Lys Leu
675 680 685

Val Phe Phe Ala Glu Asp Val Gly Ser Asn Lys Gly Ala Ile Ile Gly
690 695 700

Leu Met Val Gly Gly Val Val Ile Ala Thr Val Ile Val Ile Thr Leu
705 710 715 720

Val Met Leu Lys Lys Lys Gln Tyr Thr Ser Ile His His Gly Val Val
725 730 735

Glu Val Asp Ala Ala Val Thr Pro Glu Glu Arg His Leu Ser Lys Met
740 745 750

Gln Gln Asn Gly Tyr Glu Asn Pro Thr Tyr Lys Phe Phe Glu Gln Met
755 760 765

Gln Asn
770

<210> 56
<211> 2253
<212> DNA
<213> Homo sapiens

<400> 56
atgctgcccc gtttggcact gctcctgctg gccgcctgga cggctcgggc gctggaggta 60
cccactgatg gtaatgctgg cctgctggct gaaccccaga ttgccatgtt ctgtggcaga 120
ctgaacatgc acatgaatgt ccagaatggg aagtgggatt cagatccatc agggaccaaa 180
acctgcattg ataccaagga aggcacacct cagtattgcc aagaagtcta ccctgaactg 240
cagatcacca atgtggtaga agccaaccaa ccagtgarca tccagaactg gtgcaagcgg 300
ggccgcaagc agtgcaagac ccatcccccac tttgtgattc cctaccgctg cttagtgtgt 360
gagtttgtaa gtgatgcctt tctcgttcct gacaagtga aattcttaca ccaggagagg 420
atggatgttt gcgaaactca tcttcaactg cacaccgtcg ccaaagagac atgcagtgar 480
aagagtacca acttgcatga ctacggcatg ttgctgcctt gcggaattga caagttccga 540
ggggtagagt ttgtgtgttg cccactggct gaagaaagtg acaatgtgga ttctgctgat 600
gcgaggagg atgactcggg tgtctggtgg ggccggagcag acacagacta tgcagatggg 660
agtgaagaca aagtagtaga agtagcagag gaggaagaag tggctgagggt ggaagaagaa 720
gaagccgatg atgacgagga cgatgaggat ggtgatgagg tagaggaaga ggctgaggaa 780
ccctacgaag aagccacaga gagaaccacc agcattgcc aaccaccac caccaccaca 840
gagtctgtgg aagaggtggt tcgagaggtg tgctctgaac aagccgagac ggggccgtgc 900
cgagcaatga tctcccgtg gtactttgat gtgactgaag ggaagtgtgc cccattcitt 960
tacggcggat gtggcggcaa ccggaacaac ttgacacag aagagtactg catggccgtg 1020
tgtggcagcg ccattcctac aacagcagcc agtaccctg atgccgttga caagtatctc 1080
gagacacctg gggatgagaa tgaacatgcc catttccaga aagccaaaga gaggcttgag 1140
gccaaagcacc gagagagaat gtcccaggtc atgagagaat ggggaagaggc agaacgtcaa 1200
gcaaagaact tgcctaaagc tgataagaag gcagttatcc agcatttcca ggagaaagtg 1260
gaatctttgg aacaggaagc agccaacgag agacagcagc tgggtggagac acacatggcc 1320
agagtggaag ccattgctca tgaccgccgc cgctggccc tggagaacta catcaccgct 1380
ctgcaggctg ttctcctcgc gcctcgtcac gtgttcaata tgctaaagaa gtatgtccgc 1440
gcagaacaga aggacagaca gcacacccta aagcatttcg agcatgtgcg catggtggat 1500
cccaagaaag ccgctcagat ccggtcccag gttatgacac acctccgtgt gatttatgag 1560
cgcatgaatc agtctctctc cctgctctac aacgtgcctg cagtggccga ggagattcag 1620
gatgaagttg atgagctgct tcagaaagag caaaactatt cagatgacgt cttggccaac 1680
atgattagtg aaccaaggat cagttacgga aacgatgctc tcatgccatc tttgaccgaa 1740
acgaaaacca ccgtggagct ccttcccgtg aatggagagt tcagcctgga cgatctccag 1800
ccgtggcatt cttttggggc tgactctgtg ccagccaaca cagaaaacga agttgagcct 1860

gttgatgccc gccctgctgc cgaccgagga ctgaccactc gaccagggttc tggggttgaca 1920
 aatatcaaga cggaggagat ctctgaagtg aagatggatg cagaattccg acatgactca 1980
 ggatatgaag ttcattcatca aaaattggtg ttctttgcag aagatgtggg ttcaaacaaa 2040
 ggtgcaatca ttggactcat ggtgggcggt gttgtcatag cgacagtgat cgatcatcacc 2100
 ttgggtgatgc tgaagaagaa acagtacaca tccattcatc atgggtgtggg ggagggttgac 2160
 gccgtgtgca cccagagga gcgccacctg tccaagatgc agcagaacgg ctacgaaaat 2220
 ccaacctaca agttctttga gcagatgcag aac 2253

<210> 57
 <211> 751
 <212> PRT
 <213> Homo sapiens

<400> 57

Met Leu Pro Gly Leu Ala Leu Leu Leu Leu Ala Ala Trp Thr Ala Arg
 1 5 10 15

Ala Leu Glu Val Pro Thr Asp Gly Asn Ala Gly Leu Leu Ala Glu Pro
 20 25 30

Gln Ile Ala Met Phe Cys Gly Arg Leu Asn Met His Met Asn Val Gln
 35 40 45

Asn Gly Lys Trp Asp Ser Asp Pro Ser Gly Thr Lys Thr Cys Ile Asp
 50 55 60

Thr Lys Glu Gly Ile Leu Gln Tyr Cys Gln Glu Val Tyr Pro Glu Leu
 65 70 75 80

Gln Ile Thr Asn Val Val Glu Ala Asn Gln Pro Val Thr Ile Gln Asn
 85 90 95

Trp Cys Lys Arg Gly Arg Lys Gln Cys Lys Thr His Pro His Phe Val
 100 105 110

Ile Pro Tyr Arg Cys Leu Val Gly Glu Phe Val Ser Asp Ala Leu Leu
 115 120 125

Val Pro Asp Lys Cys Lys Phe Leu His Gln Glu Arg Met Asp Val Cys
 130 135 140

Glu Thr His Leu His Trp His Thr Val Ala Lys Glu Thr Cys Ser Glu
 145 150 155 160

Lys Ser Thr Asn Leu His Asp Tyr Gly Met Leu Leu Pro Cys Gly Ile
 165 170 175
 Asp Lys Phe Arg Gly Val Glu Phe Val Cys Cys Pro Leu Ala Glu Glu
 180 185 190
 Ser Asp Asn Val Asp Ser Ala Asp Ala Glu Glu Asp Asp Ser Asp Val
 195 200 205
 Trp Trp Gly Gly Ala Asp Thr Asp Tyr Ala Asp Gly Ser Glu Asp Lys
 210 215 220
 Val Val Glu Val Ala Glu Glu Glu Glu Val Ala Glu Val Glu Glu Glu
 225 230 235 240
 Glu Ala Asp Asp Asp Glu Asp Asp Glu Asp Gly Asp Glu Val Glu Glu
 245 250 255
 Glu Ala Glu Glu Pro Tyr Glu Glu Ala Thr Glu Arg Thr Thr Ser Ile
 260 265 270
 Ala Thr Thr Thr Thr Thr Thr Thr Glu Ser Val Glu Glu Val Val Arg
 275 280 285
 Glu Val Cys Ser Glu Gln Ala Glu Thr Gly Pro Cys Arg Ala Met Ile
 290 295 300
 Ser Arg Trp Tyr Phe Asp Val Thr Glu Gly Lys Cys Ala Pro Phe Phe
 305 310 315 320
 Tyr Gly Gly Cys Gly Gly Asn Arg Asn Asn Phe Asp Thr Glu Glu Tyr
 325 330 335
 Cys Met Ala Val Cys Gly Ser Ala Ile Pro Thr Thr Ala Ala Ser Thr
 340 345 350
 Pro Asp Ala Val Asp Lys Tyr Leu Glu Thr Pro Gly Asp Glu Asn Glu
 355 360 365
 His Ala His Phe Gln Lys Ala Lys Glu Arg Leu Glu Ala Lys His Arg
 370 375 380
 Glu Arg Met Ser Gln Val Met Arg Glu Trp Glu Glu Ala Glu Arg Gln
 385 390 395 400
 Ala Lys Asn Leu Pro Lys Ala Asp Lys Lys Ala Val Ile Gln His Phe
 405 410 415

Gln Glu Lys Val Glu Ser Leu Glu Gln Glu Ala Ala Asn Glu Arg Gln
 420 425 430

Gln Leu Val Glu Thr His Met Ala Arg Val Glu Ala Met Leu Asn Asp
 435 440 445

Arg Arg Arg Leu Ala Leu Glu Asn Tyr Ile Thr Ala Leu Gln Ala Val
 450 455 460

Pro Pro Arg Pro Arg His Val Phe Asn Met Leu Lys Lys Tyr Val Arg
 465 470 475 480

Ala Glu Gln Lys Asp Arg Gln His Thr Leu Lys His Phe Glu His Val
 485 490 495

Arg Met Val Asp Pro Lys Lys Ala Ala Gln Ile Arg Ser Gln Val Met
 500 505 510

Thr His Leu Arg Val Ile Tyr Glu Arg Met Asn Gln Ser Leu Ser Leu
 515 520 525

Leu Tyr Asn Val Pro Ala Val Ala Glu Glu Ile Gln Asp Glu Val Asp
 530 535 540

Glu Leu Leu Gln Lys Glu Gln Asn Tyr Ser Asp Asp Val Leu Ala Asn
 545 550 555 560

Met Ile Ser Glu Pro Arg Ile Ser Tyr Gly Asn Asp Ala Leu Met Pro
 565 570 575

Ser Leu Thr Glu Thr Lys Thr Thr Val Glu Leu Leu Pro Val Asn Gly
 580 585 590

Glu Phe Ser Leu Asp Asp Leu Gln Pro Trp His Ser Phe Gly Ala Asp
 595 600 605

Ser Val Pro Ala Asn Thr Glu Asn Glu Val Glu Pro Val Asp Ala Arg
 610 615 620

Pro Ala Ala Asp Arg Gly Leu Thr Thr Arg Pro Gly Ser Gly Leu Thr
 625 630 635 640

Asn Ile Lys Thr Glu Glu Ile Ser Glu Val Lys Met Asp Ala Glu Phe
 645 650 655

Arg His Asp Ser Gly Tyr Glu Val His His Gln Lys Leu Val Phe Phe
 660 665 670

Ala Glu Asp Val Gly Ser Asn Lys Gly Ala Ile Ile Gly Leu Met Val
675 680 685

Gly Gly Val Val Ile Ala Thr Val Ile Val Ile Thr Leu Val Met Leu
690 695 700

Lys Lys Lys Gln Tyr Thr Ser Ile His His Gly Val Val Glu Val Asp
705 710 715 720

Ala Ala Val Thr Pro Glu Glu Arg His Leu Ser Lys Met Gln Gln Asn
725 730 735

Gly Tyr Glu Asn Pro Thr Tyr Lys Phe Phe Glu Gln Met Gln Asn
740 745 750

<210> 58
<211> 2316
<212> DNA
<213> Homo sapiens

<400> 58
atgctgcccg gtttggcact gctcctgctg gccgcctgga cggctcgggc gctggaggta 60
cccactgatg gtaatgctgg cctgctgggt gaaccccaga ttgccatgtt ctgtggcaga 120
ctgaacatgc acatgaatgt ccagaatggg aagtgggatt cagatccatc agggacccaa 180
acctgcattg ataccaaggga aggcattcctg cagtattgcc aagaagtcta ccctgaactg 240
cagatcacca atgtggtaga agccaaccaa ccagtaccca tccagaactg gtgcaagcgg 300
ggccgcaagc agtgcaagac ccatccccac tttgtgattc cctaccgctg cttagtgtgt 360
gagtttgtaa gtgatgcctt tctcgttcct gacaagtga aattcttaca ccaggagagg 420
atggatgttt gcgaaactca tcttacttgg cacaccgtcg ccaaagagac atgcagttag 480
aagagtacca acttgcatga ctacggcatg ttgctgcctt gcggaattga caagttccga 540
ggggtagagt ttgtgtgttg cccactgggt gaagaaagtg acaatgtgga ttctgctgat 600
gcggaggagg atgactcgga tgtctgtgtg gccggagcag acacagacta tgcagatggg 660
agtgaagaca aagtagtaga agtagcagag gaggaagaag tggctgaggt ggaagaagaa 720
gaagccgatg atgacgagga cgatgaggat ggtgatgagg tagaggaaga ggctgaggaa 780
ccctacgaag aagccacaga gagaaccacc agcattgcca ccaccaccac caccaccaca 840
gagtctgtgg aagaggtggt tcgagaggtg tgctctgaac aagccgagac ggggccgtgc 900
cgagcaatga tctcccgtg gtactttgat gtgactgaag ggaagtgtgc ccatttcttt 960
tacggcggat gtggcggcaa ccggaacaac ttgacacag aagagtactg catggccgtg 1020
tgtggcagcg ccatgtccca aagtttactc aagactacc aggaacctct tggccgagat 1080
cctgttaaac ttctacaac agcagccagt acccctgatg ccgttgacaa gtatctcgag 1140

acacctgggg atgagaatga acatgccc at ttccagaaag ccaaagagag gcttgaggcc 1200
 aagcaccgag agagaatgtc ccagggtcatg agagaatggg aagaggcaga acgtcaagca 1260
 aagaacttgc ctaaagctga taagaaggca gttatccagc atttccagga gaaagtggaa 1320
 tctttggaac aggaagcagc caacgagaga cagcagctgg tggagacaca catggccaga 1380
 gtggaagcca tgctcaatga ccgcccgcgc ctggccctgg agaactacat caccgctctg 1440
 caggctgttc ctctcggcc tcgtcacgtg ttcaatatgc taaagaagta tgtccgcgca 1500
 gaacagaagg acagacagca caccctaaag catttcgagc atgtgcgcat ggtggatccc 1560
 aagaaagccg ctcatatccg gtcccagggt atgacacacc tccgtgtgat ttatgagcgc 1620
 atgaatcagt ctctctccct gctctacaac gtgcctgcag tggccgagga gattcaggat 1680
 gaagttgatg agctgcttca gaaagagcaa aactattcag atgacgtctt ggccaacatg 1740
 attagtgaac caaggatcag ttacggaaac gatgctctca tgccatcttt gaccgaaacg 1800
 aaaaccaccg tggagctcct tcccgatgaat ggagagttca gcctggacga tctccagccg 1860
 tggcattctt ttggggctga ctctgtgcca gccaacacag aaaacgaagt tgagcctgtt 1920
 gatgcccgcg ctgctgccga ccgaggactg accactcgac cagggttctgg gttgacaaat 1980
 atcaagacgg aggagatctc tgaagtgaag atggatgcag aattccgaca tgactcagga 2040
 tatgaagttc atcatcaaaa attggtgttc tttgcagaag atgtgggttc aaacaaaggt 2100
 gcaatcattg gactcatggt gggcgggtgtt gtcatagcga cagtgatcgt catcaccttg 2160
 gtgatgctga agaagaana gtacacatcc attcatcatg gtgtggtgga gggtgacgcc 2220
 gctgtcaccc cagaggagcg ccacctgtcc aagatgcagc agaacggcta cgaaaatcca 2280
 acctacaagt tctttgagca gatgcagaac aagaag 2316

<210> 59
 <211> 772
 <212> PRT
 <213> Homo sapiens

<400> 59

Met Leu Pro Gly Leu Ala Leu Leu Leu Leu Ala Ala Trp Thr Ala Arg
 1 5 10 15

Ala Leu Glu Val Pro Thr Asp Gly Asn Ala Gly Leu Leu Ala Glu Pro
 20 25 30

Gln Ile Ala Met Phe Cys Gly Arg Leu Asn Met His Met Asn Val Gln
 35 40 45

Asn Gly Lys Trp Asp Ser Asp Pro Ser Gly Thr Lys Thr Cys Ile Asp
 50 55 60

Thr Lys Glu Gly Ile Leu Gln Tyr Cys Gln Glu Val Tyr Pro Glu Leu
 65 70 75 80

Gln Ile Thr Asn Val Val Glu Ala Asn Gln Pro Val Thr Ile Gln Asn
 85 90 95

Trp Cys Lys Arg Gly Arg Lys Gln Cys Lys Thr His Pro His Phe Val
 100 105 110

Ile Pro Tyr Arg Cys Leu Val Gly Glu Phe Val Ser Asp Ala Leu Leu
 115 120 125

Val Pro Asp Lys Cys Lys Phe Leu His Gln Glu Arg Met Asp Val Cys
 130 135 140

Glu Thr His Leu His Trp His Thr Val Ala Lys Glu Thr Cys Ser Glu
 145 150 155 160

Lys Ser Thr Asn Leu His Asp Tyr Gly Met Leu Leu Pro Cys Gly Ile
 165 170 175

Asp Lys Phe Arg Gly Val Glu Phe Val Cys Cys Pro Leu Ala Glu Glu
 180 185 190

Ser Asp Asn Val Asp Ser Ala Asp Ala Glu Glu Asp Asp Ser Asp Val
 195 200 205

Trp Trp Gly Gly Ala Asp Thr Asp Tyr Ala Asp Gly Ser Glu Asp Lys
 210 215 220

Val Val Glu Val Ala Glu Glu Glu Glu Val Ala Glu Val Glu Glu Glu
 225 230 235 240

Glu Ala Asp Asp Asp Glu Asp Asp Glu Asp Gly Asp Glu Val Glu Glu
 245 250 255

Glu Ala Glu Glu Pro Tyr Glu Glu Ala Thr Glu Arg Thr Thr Ser Ile
 260 265 270

Ala Thr Thr Thr Thr Thr Thr Thr Glu Ser Val Glu Glu Val Val Arg
 275 280 285

Glu Val Cys Ser Glu Gln Ala Glu Thr Gly Pro Cys Arg Ala Met Ile
 290 295 300

Ser Arg Trp Tyr Phe Asp Val Thr Glu Gly Lys Cys Ala Pro Phe Phe
 305 310 315 320

Tyr Gly Gly Cys Gly Gly Asn Arg Asn Asn Phe Asp Thr Glu Glu Tyr
 325 330 335

Cys Met Ala Val Cys Gly Ser Ala Met Ser Gln Ser Leu Leu Lys Thr
 340 345 350

Thr Gln Glu Pro Leu Ala Arg Asp Pro Val Lys Leu Pro Thr Thr Ala
 355 360 365

Ala Ser Thr Pro Asp Ala Val Asp Lys Tyr Leu Glu Thr Pro Gly Asp
 370 375 380

Glu Asn Glu His Ala His Phe Gln Lys Ala Lys Glu Arg Leu Glu Ala
 385 390 395 400

Lys His Arg Glu Arg Met Ser Gln Val Met Arg Glu Trp Glu Glu Ala
 405 410 415

Glu Arg Gln Ala Lys Asn Leu Pro Lys Ala Asp Lys Lys Ala Val Ile
 420 425 430

Gln His Phe Gln Glu Lys Val Glu Ser Leu Glu Gln Glu Ala Ala Asn
 435 440 445

Glu Arg Gln Gln Leu Val Glu Thr His Met Ala Arg Val Glu Ala Met
 450 455 460

Leu Asn Asp Arg Arg Arg Leu Ala Leu Glu Asn Tyr Ile Thr Ala Leu
 465 470 475 480

Gln Ala Val Pro Pro Arg Pro Arg His Val Phe Asn Met Leu Lys Lys
 485 490 495

Tyr Val Arg Ala Glu Gln Lys Asp Arg Gln His Thr Leu Lys His Phe
 500 505 510

Glu His Val Arg Met Val Asp Pro Lys Lys Ala Ala Gln Ile Arg Ser
 515 520 525

Gln Val Met Thr His Leu Arg Val Ile Tyr Glu Arg Met Asn Gln Ser
 530 535 540

Leu Ser Leu Leu Tyr Asn Val Pro Ala Val Ala Glu Glu Ile Gln Asp
 545 550 555 560

Glu Val Asp Glu Leu Leu Gln Lys Glu Gln Asn Tyr Ser Asp Asp Val
 565 570 575

Leu Ala Asn Met Ile Ser Glu Pro Arg Ile Ser Tyr Gly Asn Asp Ala
 580 585 590
 Leu Met Pro Ser Leu Thr Glu Thr Lys Thr Thr Val Glu Leu Leu Pro
 595 600 605
 Val Asn Gly Glu Phe Ser Leu Asp Asp Leu Gln Pro Trp His Ser Phe
 610 615 620
 Gly Ala Asp Ser Val Pro Ala Asn Thr Glu Asn Glu Val Glu Pro Val
 625 630 635 640
 Asp Ala Arg Pro Ala Ala Asp Arg Gly Leu Thr Thr Arg Pro Gly Ser
 645 650 655
 Gly Leu Thr Asn Ile Lys Thr Glu Glu Ile Ser Glu Val Lys Met Asp
 660 665 670
 Ala Glu Phe Arg His Asp Ser Gly Tyr Glu Val His His Gln Lys Leu
 675 680 685
 Val Phe Phe Ala Glu Asp Val Gly Ser Asn Lys Gly Ala Ile Ile Gly
 690 695 700
 Leu Met Val Gly Gly Val Val Ile Ala Thr Val Ile Val Ile Thr Leu
 705 710 715 720
 Val Met Leu Lys Lys Lys Gln Tyr Thr Ser Ile His His Gly Val Val
 725 730 735
 Glu Val Asp Ala Ala Val Thr Pro Glu Glu Arg His Leu Ser Lys Met
 740 745 750
 Gln Gln Asn Gly Tyr Glu Asn Pro Thr Tyr Lys Phe Phe Glu Gln Met
 755 760 765
 Gln Asn Lys Lys
 770

<210> 60
 <211> 2259
 <212> DNA
 <213> Homo sapiens

<400> 60
 atgctgcccc gtttggcact gtcctgctg gccgcctgga cggctcgggc gctggaggta 60
 ccactgatg gtaatgctgg cctgctggct gaaccccaga ttgccatgtt ctgtggcaga 120
 ctgaacatgc acatgaatgt ccagaatggg aagtgggatt cagatccatc agggacacaaa 180

acctgcattg	ataccaagga	aggcatcctg	cagtattgcc	aagaagtcta	ccctgaactg	240
cagatcacca	atgtggtaga	agccaaccaa	ccagtgacca	tccagaactg	gtgcaagcgg	300
ggccgcaagc	agtgaagac	ccatccccac	tttgtgattc	cctaccgctg	cttagttggt	360
gagtttgtaa	gtgatgcctt	tctcgttcct	gacaagtgca	aattcttaca	ccaggagagg	420
atggatgttt	gcgaaactca	tcttcactgg	cacaccgtcg	ccaaagagac	atgcagtgag	480
aagagtacca	acttgcata	ctacggcatg	ttgctgcctt	gcggaattga	caagttccga	540
ggggtagagt	ttgtgtgttg	cccactggct	gaagaaagtg	acaatgtgga	ttctgctgat	600
gcggaggagg	atgactcgga	tgtctggtgg	ggcggagcag	acacagacta	tgcagatggg	660
agtgaagaca	aagtagtaga	agtagcagag	gaggaagaag	tggctgaggt	ggaagaagaa	720
gaagccgatg	atgacgagga	cgatgaggat	ggtgatgagg	tagaggaaga	ggctgaggaa	780
ccctacgaag	aagccacaga	gagaaccacc	agcattgcc	ccaccaccac	caccaccaca	840
gagtctgtgg	aagaggtggt	tcgagagggt	tgctctgaac	aagccgagac	ggggccgtgc	900
cgagcaatga	tctcccgtg	gtactttgat	gtgactgaag	ggaagtgtgc	cccattcttt	960
tacggcggat	gtggcggcaa	ccggaacaac	tttgacacag	aagagtactg	catggccgtg	1020
tgtggcagcg	ccattcctac	aacagcagcc	agtaccctg	atgccgttga	caagtatctc	1080
gagacacctg	gggatgagaa	tgaacatgcc	catttccaga	aagccaaaga	gaggetttag	1140
gccaagcacc	gagagagaat	gtcccagggtc	atgagagaat	gggaagaygc	agaacgtcaa	1200
gcaaagaact	tgcctaaagc	tgataagaag	gcagttatcc	agcatttcca	ggagaaagtg	1260
gaatcttttg	aacaggaagc	agccaacgag	agacagcagc	tggtggagac	acacatggcc	1320
agagtggaa	ccatgctcaa	tgaccgccgc	cgctggccc	tggagaacta	catcaccgct	1380
ctgcaggctg	ttcctcctcg	gcctcgtcac	gtgttcaata	tgctaaagaa	gtatgtccgc	1440
gcagaacaga	aggacagaca	gcacacccta	aagcatttcg	agcatgtgcg	catggtggat	1500
ccaagaaag	ccgctcagat	ccggtcccag	gttatgacac	acctccgtgt	gatttatgag	1560
cgcataatc	agtctctctc	cctgctctac	aacgtgcctg	cagtggccga	ggagattcag	1620
gatgaagttg	atgagctgct	tcagaaagag	caaaactatt	cagatgacgt	cttggccaac	1680
atgattagt	aaccaaggat	cagttacgga	aacgatgctc	tcatgccatc	tttgaccgaa	1740
acgaaaacca	ccgtggagct	ccttcccgtg	aatggagagt	tcagcctgga	cgatctccag	1800
ccgtggcatt	cttttggggc	tgactctgtg	ccagccaaca	cagaaaacga	agttgagcct	1860
gttgatgccc	gccctgctgc	cgaccgagga	ctgaccactc	gaccagggttc	tgggttgaca	1920
aatatcaaga	cggaggagat	ctctgaagt	aagatggatg	cagaattccg	acatgactca	1980
ggatatgaag	ttcatcatca	aaaattggtg	ttctttgcag	aagatgtggg	ttcaaacaaa	2040
ggtgcaatca	ttggactcat	ggtgggcggg	gttgtcatag	cgacagtgat	cgatcatcacc	2100

ttggtgatgc tgaagaagaa acagtacaca tccattcatc atggtgtggt ggaggttgac 2160
 gccgctgtca cccagagga gcgccacctg tccaagatgc agcagaacgg ctacgaaaat 2220
 ccaacctaca agttctttga gcagatgcag aacaagaag 2259

<210> 61
 <211> 753
 <212> PRT
 <213> Homo sapiens

<400> 61

Met Leu Pro Gly Leu Ala Leu Leu Leu Ala Ala Trp Thr Ala Arg
 1 5 10 15

Ala Leu Glu Val Pro Thr Asp Gly Asn Ala Gly Leu Leu Ala Glu Pro
 20 25 30

Gln Ile Ala Met Phe Cys Gly Arg Leu Asn Met His Met Asn Val Gln
 35 40 45

Asn Gly Lys Trp Asp Ser Asp Pro Ser Gly Thr Lys Thr Cys Ile Asp
 50 55 60

Thr Lys Glu Gly Ile Leu Gln Tyr Cys Gln Glu Val Tyr Pro Glu Leu
 65 70 75 80

Gln Ile Thr Asn Val Val Glu Ala Asn Gln Pro Val Thr Ile Gln Asn
 85 90 95

Trp Cys Lys Arg Gly Arg Lys Gln Cys Lys Thr His Pro His Phe Val
 100 105 110

Ile Pro Tyr Arg Cys Leu Val Gly Glu Phe Val Ser Asp Ala Leu Leu
 115 120 125

Val Pro Asp Lys Cys Lys Phe Leu His Gln Glu Arg Met Asp Val Cys
 130 135 140

Glu Thr His Leu His Trp His Thr Val Ala Lys Glu Thr Cys Ser Glu
 145 150 155 160

Lys Ser Thr Asn Leu His Asp Tyr Gly Met Leu Leu Pro Cys Gly Ile
 165 170 175

Asp Lys Phe Arg Gly Val Glu Phe Val Cys Cys Pro Leu Ala Glu Glu
 180 185 190

Ser Asp Asn Val Asp Ser Ala Asp Ala Glu Glu Asp Asp Ser Asp Val
 195 200 205

Trp Trp Gly Gly Ala Asp Thr Asp Tyr Ala Asp Gly Ser Glu Asp Lys
 210 215 220

Val Val Glu Val Ala Glu Glu Glu Glu Val Ala Glu Val Glu Glu Glu
 225 230 235 240

Glu Ala Asp Asp Asp Glu Asp Asp Glu Asp Gly Asp Glu Val Glu Glu
 245 250 255

Glu Ala Glu Glu Pro Tyr Glu Glu Ala Thr Glu Arg Thr Thr Ser Ile
 260 265 270

Ala Thr Thr Thr Thr Thr Thr Thr Glu Ser Val Glu Glu Val Val Arg
 275 280 285

Glu Val Cys Ser Glu Gln Ala Glu Thr Gly Pro Cys Arg Ala Met Ile
 290 295 300

Ser Arg Trp Tyr Phe Asp Val Thr Glu Gly Lys Cys Ala Pro Phe Phe
 305 310 315 320

Tyr Gly Gly Cys Gly Gly Asn Arg Asn Asn Phe Asp Thr Glu Glu Tyr
 325 330 335

Cys Met Ala Val Cys Gly Ser Ala Ile Pro Thr Thr Ala Ala Ser Thr
 340 345 350

Pro Asp Ala Val Asp Lys Tyr Leu Glu Thr Pro Gly Asp Glu Asn Glu
 355 360 365

His Ala His Phe Gln Lys Ala Lys Glu Arg Leu Glu Ala Lys His Arg
 370 375 380

Glu Arg Met Ser Gln Val Met Arg Glu Trp Glu Glu Ala Glu Arg Gln
 385 390 395 400

Ala Lys Asn Leu Pro Lys Ala Asp Lys Lys Ala Val Ile Gln His Phe
 405 410 415

Gln Glu Lys Val Glu Ser Leu Glu Gln Glu Ala Ala Asn Glu Arg Gln
 420 425 430

Gln Leu Val Glu Thr His Met Ala Arg Val Glu Ala Met Leu Asn Asp
 435 440 445

Arg Arg Arg Leu Ala Leu Glu Asn Tyr Ile Thr Ala Leu Gln Ala Val
 450 455 460

Pro Pro Arg Pro Arg His Val Phe Asn Met Leu Lys Lys Tyr Val Arg
 465 470 475 480

Ala Glu Gln Lys Asp Arg Gln His Thr Leu Lys His Phe Glu His Val
 485 490 495

Arg Met Val Asp Pro Lys Lys Ala Ala Gln Ile Arg Ser Gln Val Met
 500 505 510

Thr His Leu Arg Val Ile Tyr Glu Arg Met Asn Gln Ser Leu Ser Leu
 515 520 525

Leu Tyr Asn Val Pro Ala Val Ala Glu Glu Ile Gln Asp Glu Val Asp
 530 535 540

Glu Leu Leu Gln Lys Glu Gln Asn Tyr Ser Asp Asp Val Leu Ala Asn
 545 550 555 560

Met Ile Ser Glu Pro Arg Ile Ser Tyr Gly Asn Asp Ala Leu Met Pro
 565 570 575

Ser Leu Thr Glu Thr Lys Thr Thr Val Glu Leu Leu Pro Val Asn Gly
 580 585 590

Glu Phe Ser Leu Asp Asp Leu Gln Pro Trp His Ser Phe Gly Ala Asp
 595 600 605

Ser Val Pro Ala Asn Thr Glu Asn Glu Val Glu Pro Val Asp Ala Arg
 610 615 620

Pro Ala Ala Asp Arg Gly Leu Thr Thr Arg Pro Gly Ser Gly Leu Thr
 625 630 635 640

Asn Ile Lys Thr Glu Glu Ile Ser Glu Val Lys Met Asp Ala Glu Phe
 645 650 655

Arg His Asp Ser Gly Tyr Glu Val His His Gln Lys Leu Val Phe Phe
 660 665 670

Ala Glu Asp Val Gly Ser Asn Lys Gly Ala Ile Ile Gly Leu Met Val
 675 680 685

Gly Gly Val Val Ile Ala Thr Val Ile Val Ile Thr Leu Val Met Leu
 690 695 700

Lys Lys Lys Gln Tyr Thr Ser Ile His His Gly Val Val Glu Val Asp
705 710 715 720

Ala Ala Val Thr Pro Glu Glu Arg His Leu Ser Lys Met Gln Gln Asn
725 730 735

Gly Tyr Glu Asn Pro Thr Tyr Lys Phe Phe Glu Gln Met Gln Asn Lys
740 745 750

Lys

<210> 62
<211> 8
<212> PRT
<213> Artificial sequence

<220>
<223> Synthetic peptide

<400> 62

Leu Glu Val Leu Phe Gln Gly Pro
1 5

<210> 63
<211> 10
<212> PRT
<213> Artificial sequence

<220>
<223> Synthetic peptide

<400> 63

Ser Glu Val Asn Leu Asp Ala Glu Phe Arg
1 5 10

<210> 64
<211> 10
<212> PRT
<213> Artificial sequence

<220>
<223> Synthetic peptide

<400> 64

Ser Glu Val Lys Met Asp Ala Glu Phe Arg
1 5 10

<210> 65
<211> 15
<212> PRT
<213> Artificial sequence

<220>

<223> Synthetic peptide

<400> 65

Arg Arg Gly Gly Val Val Ile Ala Thr Val Ile Val Gly Glu Arg
1 5 10 15

<210> 66

<211> 518

<212> PRT

<213> Homo sapiens

<400> 66

Met Gly Ala Leu Ala Arg Ala Leu Leu Leu Pro Leu Leu Ala Gln Trp
1 5 10 15

Leu Leu Arg Ala Ala Pro Glu Leu Ala Pro Ala Pro Phe Thr Leu Pro
20 25 30

Leu Arg Val Ala Ala Ala Thr Asn Arg Val Val Ala Pro Thr Pro Gly
35 40 45

Pro Gly Thr Pro Ala Glu Arg His Ala Asp Gly Leu Ala Leu Ala Leu
50 55 60

Glu Pro Ala Leu Ala Ser Pro Ala Gly Ala Ala Asn Phe Leu Ala Met
65 70 75 80

Val Asp Asn Leu Gln Gly Asp Ser Gly Arg Gly Tyr Tyr Leu Glu Met
85 90 95

Leu Ile Gly Thr Pro Pro Gln Lys Leu Gln Ile Leu Val Asp Thr Gly
100 105 110

Ser Ser Asn Phe Ala Val Ala Gly Thr Pro His Ser Tyr Ile Asp Thr
115 120 125

Tyr Phe Asp Thr Glu Arg Ser Ser Thr Tyr Arg Ser Lys Gly Phe Asp
130 135 140

Val Thr Val Lys Tyr Thr Gln Gly Ser Trp Thr Gly Phe Val Gly Glu
145 150 155 160

Asp Leu Val Thr Ile Pro Lys Gly Phe Asn Thr Ser Phe Leu Val Asn
165 170 175

Ile Ala Thr Ile Phe Glu Ser Glu Asn Phe Phe Leu Pro Gly Ile Lys
180 185 190

Trp Asn Gly Ile Leu Gly Leu Ala Tyr Ala Thr Leu Ala Lys Pro Ser
 195 200 205
 Ser Ser Leu Glu Thr Phe Phe Asp Ser Leu Val Thr Gln Ala Asn Ile
 210 215 220
 Pro Asn Val Phe Ser Met Gln Met Cys Gly Ala Gly Leu Pro Val Ala
 225 230 235 240
 Gly Ser Gly Thr Asn Gly Gly Ser Leu Val Leu Gly Gly Ile Glu Pro
 245 250 255
 Ser Leu Tyr Lys Gly Asp Ile Trp Tyr Thr Pro Ile Lys Glu Glu Trp
 260 265 270
 Tyr Tyr Gln Ile Glu Ile Leu Lys Leu Glu Ile Gly Gly Gln Ser Leu
 275 280 285
 Asn Leu Asp Cys Arg Glu Tyr Asn Ala Asp Lys Ala Ile Val Asp Ser
 290 295 300
 Gly Thr Thr Leu Leu Arg Leu Pro Gln Lys Val Phe Asp Ala Val Val
 305 310 315 320
 Glu Ala Val Ala Arg Ala Ser Leu Ile Pro Glu Phe Ser Asp Gly Phe
 325 330 335
 Trp Thr Gly Ser Gln Leu Ala Cys Trp Thr Asn Ser Glu Thr Pro Trp
 340 345 350
 Ser Tyr Phe Pro Lys Ile Ser Ile Tyr Leu Arg Asp Glu Asn Ser Ser
 355 360 365
 Arg Ser Phe Arg Ile Thr Ile Leu Pro Gln Leu Tyr Ile Gln Pro Met
 370 375 380
 Met Gly Ala Gly Leu Asn Tyr Glu Cys Tyr Arg Phe Gly Ile Ser Pro
 385 390 395 400
 Ser Thr Asn Ala Leu Val Ile Gly Ala Thr Val Met Glu Gly Phe Tyr
 405 410 415
 Val Ile Phe Asp Arg Ala Gln Lys Arg Val Gly Phe Ala Ala Ser Pro
 420 425 430
 Cys Ala Glu Ile Ala Gly Ala Ala Val Ser Glu Ile Ser Gly Pro Phe
 435 440 445

Ser Thr Glu Asp Val Ala Ser Asn Cys Val Pro Ala Gln Ser Leu Ser
450 455 460

Glu Pro Ile Leu Trp Ile Val Ser Tyr Ala Leu Met Ser Val Cys Gly
465 470 475 480

Ala Ile Leu Leu Val Leu Ile Val Leu Leu Leu Pro Phe Arg Cys
485 490 495

Gln Arg Arg Pro Arg Asp Pro Glu Val Val Asn Asp Glu Ser Ser Leu
500 505 510

Val Arg His Arg Trp Lys
515

<210> 67
<211> 475
<212> PRT
<213> Homo sapiens

<400> 67

Met Gly Ala Leu Ala Arg Ala Leu Leu Leu Pro Leu Leu Ala Gln Trp
1 5 10 15

Leu Leu Arg Ala Ala Pro Glu Leu Ala Pro Ala Pro Phe Thr Leu Pro
20 25 30

Leu Arg Val Ala Ala Ala Thr Asn Arg Val Val Ala Pro Thr Pro Gly
35 40 45

Pro Gly Thr Pro Ala Glu Arg His Ala Asp Gly Leu Ala Leu Ala Leu
50 55 60

Glu Pro Ala Leu Ala Ser Pro Ala Gly Ala Ala Asn Phe Leu Ala Met
65 70 75 80

Val Asp Asn Leu Gln Gly Asp Ser Gly Arg Gly Tyr Tyr Leu Glu Met
85 90 95

Leu Ile Gly Thr Pro Pro Gln Lys Leu Gln Ile Leu Val Asp Thr Gly
100 105 110

Ser Ser Asn Phe Ala Val Ala Gly Thr Pro His Ser Tyr Ile Asp Thr
115 120 125

Tyr Phe Asp Thr Glu Arg Ser Ser Thr Tyr Arg Ser Lys Gly Phe Asp
130 135 140

Val Thr Val Lys Tyr Thr Gln Gly Ser Trp Thr Gly Phe Val Gly Glu
 145 150 155 160
 Asp Leu Val Thr Ile Pro Lys Gly Phe Asn Thr Ser Phe Leu Val Asn
 165 170 175
 Ile Ala Thr Ile Phe Glu Ser Glu Asn Phe Phe Leu Pro Gly Ile Lys
 180 185 190
 Trp Asn Gly Ile Leu Gly Leu Ala Tyr Ala Thr Leu Ala Lys Pro Ser
 195 200 205
 Ser Ser Leu Glu Thr Phe Phe Asp Ser Leu Val Thr Gln Ala Asn Ile
 210 215 220
 Pro Asn Val Phe Ser Met Gln Met Cys Gly Ala Gly Leu Pro Val Ala
 225 230 235 240
 Gly Ser Gly Thr Asn Gly Gly Ser Leu Val Leu Gly Gly Ile Glu Pro
 245 250 255
 Ser Leu Tyr Lys Gly Asp Ile Trp Tyr Thr Pro Ile Lys Glu Glu Trp
 260 265 270
 Tyr Tyr Gln Ile Glu Ile Leu Lys Leu Glu Ile Gly Gly Gln Ser Leu
 275 280 285
 Asn Leu Asp Cys Arg Glu Tyr Asn Ala Asp Lys Ala Ile Val Asp Ser
 290 295 300
 Gly Thr Thr Leu Leu Arg Leu Pro Gln Lys Val Phe Asp Ala Val Val
 305 310 315 320
 Glu Ala Val Ala Arg Ala Ser Leu Ile Pro Glu Phe Ser Asp Gly Phe
 325 330 335
 Trp Thr Gly Ser Gln Leu Ala Cys Trp Thr Asn Ser Glu Thr Pro Trp
 340 345 350
 Ser Tyr Phe Pro Lys Ile Ser Ile Tyr Leu Arg Asp Glu Asn Ser Ser
 355 360 365
 Arg Ser Phe Arg Ile Thr Ile Leu Pro Gln Leu Tyr Ile Gln Pro Met
 370 375 380
 Met Gly Ala Gly Leu Asn Tyr Glu Cys Tyr Arg Phe Gly Ile Ser Pro
 385 390 395 400

Ser Thr Asn Ala Leu Val Ile Gly Ala Thr Val Met Glu Gly Phe Tyr
405 410 415

Val Ile Phe Asp Arg Ala Gln Lys Arg Val Gly Phe Ala Ala Ser Pro
420 425 430

Cys Ala Glu Ile Ala Gly Ala Ala Val Ser Glu Ile Ser Gly Pro Phe
435 440 445

Ser Thr Glu Asp Val Ala Ser Asn Cys Val Pro Ala Gln Ser Leu Ser
450 455 460

Glu Pro Ile Leu Trp His His His His His His
465 470 475

<210> 68
<211> 413
<212> PRT
<213> Homo sapiens

<400> 68

Ala Leu Glu Pro Ala Leu Ala Ser Pro Ala Gly Ala Ala Asn Phe Leu
1 5 10 15

Ala Met Val Asp Asn Leu Gln Gly Asp Ser Gly Arg Gly Tyr Tyr Leu
20 25 30

Glu Met Leu Ile Gly Thr Pro Pro Gln Lys Leu Gln Ile Leu Val Asp
35 40 45

Thr Gly Ser Ser Asn Phe Ala Val Ala Gly Thr Pro His Ser Tyr Ile
50 55 60

Asp Thr Tyr Phe Asp Thr Glu Arg Ser Ser Thr Tyr Arg Ser Lys Gly
65 70 75 80

Phe Asp Val Thr Val Lys Tyr Thr Gln Gly Ser Trp Thr Gly Phe Val
85 90 95

Gly Glu Asp Leu Val Thr Ile Pro Lys Gly Phe Asn Thr Ser Phe Leu
100 105 110

Val Asn Ile Ala Thr Ile Phe Glu Ser Glu Asn Phe Phe Leu Pro Gly
115 120 125

Ile Lys Trp Asn Gly Ile Leu Gly Leu Ala Tyr Ala Thr Leu Ala Lys
130 135 140

Pro Ser Ser Ser Leu Glu Thr Phe Phe Asp Ser Leu Val Thr Gln Ala
 145 150 155 160

Asn Ile Pro Asn Val Phe Ser Met Gln Met Cys Gly Ala Gly Leu Pro
 165 170 175

Val Ala Gly Ser Gly Thr Asn Gly Gly Ser Leu Val Leu Gly Gly Ile
 180 185 190

Glu Pro Ser Leu Tyr Lys Gly Asp Ile Trp Tyr Thr Pro Ile Lys Glu
 195 200 205

Glu Trp Tyr Tyr Gln Ile Glu Ile Leu Lys Leu Glu Ile Gly Gly Gln
 210 215 220

Ser Leu Asn Leu Asp Cys Arg Glu Tyr Asn Ala Asp Lys Ala Ile Val
 225 230 235 240

Asp Ser Gly Thr Thr Leu Leu Arg Leu Pro Gln Lys Val Phe Asp Ala
 245 250 255

Val Val Glu Ala Val Ala Arg Ala Ser Leu Ile Pro Glu Phe Ser Asp
 260 265 270

Gly Phe Trp Thr Gly Ser Gln Leu Ala Cys Trp Thr Asn Ser Glu Thr
 275 280 285

Pro Trp Ser Tyr Phe Pro Lys Ile Ser Ile Tyr Leu Arg Asp Glu Asn
 290 295 300

Ser Ser Arg Ser Phe Arg Ile Thr Ile Leu Pro Gln Leu Tyr Ile Gln
 305 310 315 320

Pro Met Met Gly Ala Gly Leu Asn Tyr Glu Cys Tyr Arg Phe Gly Ile
 325 330 335

Ser Pro Ser Thr Asn Ala Leu Val Ile Gly Ala Thr Val Met Glu Gly
 340 345 350

Phe Tyr Val Ile Phe Asp Arg Ala Gln Lys Arg Val Gly Phe Ala Ala
 355 360 365

Ser Pro Cys Ala Glu Ile Ala Gly Ala Ala Val Ser Glu Ile Ser Gly
 370 375 380

Pro Phe Ser Thr Glu Asp Val Ala Ser Asn Cys Val Pro Ala Gln Ser
 385 390 395 400

Leu Ser Glu Pro Ile Leu Trp His His His His His
405 410

<210> 69
<211> 8
<212> PRT
<213> Artificial sequence

<220>
<223> Synthetic peptide

<400> 69

Gly Leu Ala Leu Ala Leu Glu Pro
1 5

<210> 70
<211> 8
<212> PRT
<213> Artificial sequence

<220>
<223> Synthetic peptide

<400> 70

Glu Val Lys Met Asp Ala Glu Phe
1 5

<210> 71
<211> 8
<212> PRT
<213> Artificial sequence

<220>
<223> Synthetic peptide

<400> 71

Glu Val Asn Leu Asp Ala Glu Phe
1 5

<210> 72
<211> 8
<212> PRT
<213> Artificial sequence

<220>
<223> Synthetic peptide

<400> 72

Leu Val Phe Phe Ala Glu Asp Val
1 5

<210> 73
<211> 8
<212> PRT
<213> Artificial sequence

<220>
<223> Synthetic peptide

<400> 73

Lys Leu Val Phe Phe Ala Glu Asp
1 5

<210> 74
<211> 39
<212> DNA
<213> Artificial sequence

<220>
<223> Primer

<400> 74
cgctttaagc ttgccaccat gggcgactg gcccgggcg

39

<210> 75
<211> 57
<212> DNA
<213> Artificial sequence

<220>
<223> Primer

<400> 75
cgctttctcg agctaattggt gatggtgatg gtgccacaaa atgggctcgc tcaaaga

57

<210> 76
<211> 4
<212> PRT
<213> Artificial sequence

<220>
<223> Synthetic peptide

<400> 76

Asn Leu Asp Ala
1

<210> 77
<211> 5
<212> PRT
<213> Artificial sequence

<220>
<223> Synthetic peptide

<400> 77

Gly Arg Arg Gly Ser
1 5

<210> 78
<211> 6
<212> PRT
<213> Artificial sequence

<220>
<223> Synthetic peptide

<400> 78

Thr Gln His Gly Ile Arg
1 5

<210> 79
<211> 6
<212> PRT
<213> Artificial sequence

<220>
<223> Synthetic peptide

<400> 79

Glu Thr Asp Glu Glu Pro
1 5

<210> 80
<211> 15
<212> PRT
<213> Artificial sequence

<220>
<223> Synthetic peptide

<400> 80

Met Cys Ala Glu Val Lys Met Asp Ala Glu Phe Lys Asp Asn Pro
1 5 10 15

<210> 81
<211> 5
<212> PRT
<213> Artificial sequence

<220>
<223> Synthetic peptide

<400> 81

Asp Ala Glu Phe Arg
1 5

<210> 82
<211> 5
<212> PRT
<213> Artificial sequence

<220>
<223> Synthetic peptide

<400> 82

Ser Glu Val Asn Leu
1 5

<210> 83
<211> 4
<212> PRT
<213> Artificial sequence

<220>
<223> Peptide of Human APP

<220>
<221> misc_feature
<222> (1)
<223> Xaa = Lys or Asn

<220>
<221> misc_feature
<222> (2)
<223> Xaa = Met or Leu

<220>
<221> misc_feature
<222> (3)
<223> Xaa = Asp

<220>
<221> misc_feature
<222> (4)
<223> Xaa = Asp

<400> 83

Xaa Xaa Xaa Xaa
1

FIGURE 1 (1)

ATGGGCGCACTGGCCCCGGGCGCTGCTGCTGCTGCTGCTGGCCCAGTGGCTCCTGCGCGCC
 M G A L A R A L L L P L L A Q W L L R A

 CCCCCGAGCTGGCCCCCGCGCCCTTCACGCTGCCCCCTCCGGGTGGCCGCGGCCACGAAC
 A P E L A P A P F T L P L R V A A A T N

 CGCGTAGTTGCGCCACCCCGGGACCCGGGACCCCTGCCGAGCGCCACGCCGACGGCTTG
 R V V A P T P G P G T P A E R H A D G L

 GCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCCGGGCGCCGCCAACTTCTTGCCATG
 A L A L E P A L A S P A G A A N F L A M

 GTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACTACCTGGAGATGCTGATCGGGACC
 V D N L Q G D S G R G Y Y L E M L I G T

 CCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTAACCTTGCCGTGGCAGGA
 P P Q K L Q I L V D T G S S N F A V A G

 ACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGTCTAGCACATACCGCTCC
 T P H S Y I D T Y F D T E R S S T Y R S

 AAGGGCTTTGACGTCACAGTGAAGTACACAAGGAAGCTGGACGGGCTTCGTTGGGGAA
 K G F D V T V K Y T Q G S W T G F V G E

 GACCTCGTCACCATCCCCAAAGGCTTCAATACITCTTTTCTTGTCAACATTGCCACTATT
 D L V T I P K G F N T S F L V N I A T I

 TTTGAATCAGAGAATTTCTTTTGGCTGGGATTAAATGGAATGGAATACTTGGCCTAGCT
 F E S E N F F L P G I K W N G I L G L A

 TATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTGACA
 Y A T L A K P S S S L E T F F D S L V T

 CAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCCGTGCT
 Q A N I P N V F S M Q M C G A G L P V A

 GGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGTATAAA
 G S G T N G G S L V L G G I E P S L Y K

 GGAGACATCTGGTATACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTTCTGAAA
 G D I W Y T P I K E E W Y Y Q I E I L K

 TTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGCC
 L E I G G Q S L N L D C R E Y N A D K A

 ATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTG
 I V D S G T T L L R L P Q K V F D A V V

 GAAGCTGTGGCCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCC
 E A V A R A S L I P E F S D G F W T G S

 CAGCTGGCGTGCTGGACGAATTCGGAAACACCTTGGTCTTACTTCCCTAAAATCTCCATC
 Q L A C W T N S E T P W S Y F P K I S I

 TACCTGAGAGATGAGAACTCCAGCAGGTCAATTCGATATCACAATCCTGCCTCAGCTTTAC
 Y L R D E N S S R S F R I T I L P Q L Y

 ATTCAGCCCATGATGGGGGCGGCTGAATTATGAATGTTACCGATTCCGGCATTTCCTCCA
 I Q P M M G A G L N Y E C Y R F G I S P

002250" + TE89950

TCCACAAATGCGCTGGTGATCGGTGCCACGGTGATGGAGGGCTTCTACGTCATCTTCGAC
S T N A L V I G A T V M E G F Y V I F D
AGAGCCCAGAAGAGGGTGGGCTTCGCAGCGAGCCCCCTGTGCAGAAATTGCAGGTGCTGCA

096634.092200

FIGURE 1 (2)

R A Q K R V G F A A S P C A E I A G A A
GTGTCTGAAATTTCCGGGCCCTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCCGCT
V S E I S G P F S T E D V A S N C V P A
CAGTCTTTGAGCGAGCCCATTTTGTGGATTGTGTCTATGCGCTCATGAGCGTCTGTGGA
Q S L S E P I L W I V S Y A L M S V C G
GCCATCCTCCTTGTCTTAATCGTCCTGCTGCTGCTGCCGTTCCGGTGTCAGCGTCGCCCC
A I L L V L I V L L L L P F R C Q R R P
CGTGACCCTGAGGTCGTCAATGATGAGTCCTCTCTGGTCAGACATCGCTGGAAATGAATA
R D P E V V N D E S S L V R H R W K
GCCAGGCCTGACCTCAAGCAACCATGAACTCAGCTATTAAGAAAATCACATTTCCAGGGC
AGCAGCCGGGATCGATGGTGGCGCTTTCTCCTGTGCCCACCCGTCTTCAATCTCTGTTCT
GCTCCCAGATGCCTTCTAGATTCACTGTCTTTTGATTCTTGATTTTCAAGCTTTCAAATC
CTCCCTACTTCCAAGAAAAATAATTAACAAAAAACTTCATTCTAAACCAAAAAAAAAA
AAAA

FIGURE 2 (1)

ATGGCCCAAGCCCTGCCCTGGCTCCTGCTGTGGATGGGCGCGGGAGTGCTGCCTGCCAC
 M A Q A L P W L L L W M G A G V L P A H
 GGCACCCAGCACGGCATCCGGCTGCCCTGCGCAGCGGCCTGGGGGGCGCCCCCTGGGG
 G T Q H G I R L P L R S G L G G A P L G
 CTGCGGCTGCCCCGGGAGACCGACGAAGAGCCCCGAGGAGCCCGGCCGGAGGGGCAGCTTT
 L R L P R E T D E E P E E P G R R G S F
 GTGGAGATGGTGGACAACCTGAGGGGCAAGTCGGGGCAGGGCTACTACGTGGAGATGACC
 V E M V D N L R G K S G Q G Y Y V E M T
 GTGGGCAGCCCCCGCAGACGCTCAACATCCTGGTGGATACAGGCAGCAGTAACCTTTGCA
 V G S P P Q T L N I L V D T G S S N F A
 GTGGGTGCTGCCCCCACCCCTTCCTGCATCGCTACTACCAGAGGCAGCTGTCCAGCACA
 V G A A P H P F L H R Y Y Q R Q L S S T
 TACCGGGACCTCCGGAAGGGTGTGTATGTGCCCTACACCCAGGGCAAGTGGGAAGGGGAG
 Y R D L R K G V Y V P Y T Q G K W E G E
 CTGGGCACCGACCTGGTAAGCATCCCCATGGCCCCAACGTCACTGTGCGTGCCAACATT
 L G T D L V S I P H G P N V T V R A N I
 GCTGCCATCACTGAATCAGACAAGTTCTTCATCAACGGCTCCAAGTGGGAAGGCATCCTG
 A A I T E S D K F F I N G S N W E G I L
 GGGCTGGCCTATGCTGAGATTGCCAGGCTTTGTGGTGCTGGCTTCCCCCTCAACCAAGTCT
 G L A Y A E I A R L C G A G F P L N Q S
 GAAGTGCTGGCCTCTGTGCGAGGGAGCATGATCATTGGAGGTATCGACCACTCGCTGTAC
 E V L A S V G G S M I I G G I D H S L Y
 ACAGGCAGTCTCTGGTATACACCCATCCGGCGGGAGTGGTATTATGAGGTGATCATTGTG
 T G S L W Y T P I R R E W Y Y E V I I V
 CGGGTGGAGATCAATGGACAGGATCTGAAAATGGACTGCAAGGAGTACAACCTATGACAAG
 R V E I N G Q D L K M D C K E Y N Y D K
 AGCATTGTGGACAGTGGCACCACCAACCTTCGTTTGCCCAAGAAAGTGTGTTGAAGCTGCA
 S I V D S G T T N L R L P K K V F E A A
 GTCAAATCCATCAAGGCAGCCTCCTCCACGGAGAAGTTCCTGATGGTTTCTGGCTAGGA
 V K S I K A A S S T E K F P D G F W L G
 GAGCAGCTGGTGTGCTGGCAAGCAGGCACCACCCCTTGGAACATTTTCCCAGTCATCTCA
 E Q L V C W Q A G T T P W N I F P V I S
 CTCTACCTAATGGGTGAGGTTACCAACCAGTCCTTCCGCATCACCATCCTTCCGCAGCAA
 L Y L M G E V T N Q S F R I T I L P Q Q
 TACCTGCGGCCAGTGGAAGATGTGGCCACGTCCCAAGACGACTGTTACAAGTTTGCCATC

FIGURE 2 (2)

Y L R P V E D V A T S Q D D C Y K F A I
 TCACAGTCATCCACGGGCACTGTTATGGGAGCTGTTATCATGGAGGGCTTCTACGTTGTC
 S Q S S T G T V M G A V I M E G F Y V V
 TTTGATCGGGCCCGAAAACGAATTGGCTTTGCTGTCAGCGCTTGCCATGTGCACGATGAG
 F D R A R K R I G F A V S A C H V H D E
 TTCAGGACGGCAGCGGTGGAAGGCCCTTTTGTACCTTGACATGGAAGACTGTGGCTAC
 F R T A A V E G P F V T L D M E D C G Y
 AACATTCCACAGACAGATGAGTCAACCCTCATGACCATAGCCTATGTATGGCTGCCATC
 N I P Q T D E S T L M T I A Y V M A A I
 TGCGCCCTCTTCATGCTGCCACTCTGCCTCATGGTGTGTCAGTGGCGCTGCCTCCGCTGC
 C A L F M L P L C L M V C Q W R C L R C
 CTGCGCCAGCAGCATGATGACTTTGCTGATGACATCTCCCTGCTGAAGTGAGGAGGCCCA
 L R Q Q H D D F A D D I S L L K
 TGGGCAGAAGATAGAGATTCCCCTGGACCACACCTCCGTGGTTCACTTTGGTCACAAGTA
 GGAGACACAGATGGCACCTGTGGCCAGAGCACCTCAGGACCCTCCCCACCCACCAAAATGC
 CTCTGCCTTGATGGAGAAGGAAAAGGCTGGCAAGGTGGGTTCCAGGGACTGTACCTGTAG
 GAAACAGAAAAGAGAAGAAAGAAGCACTCTGCTGGCGGGAATACTCTTGGTCACCTCAA
 TTAAAGTCGGGAAATTCTGCTGCTTGAACTTCAGCCCTGAACCTTTGTCCACCATTCCT
 TTAAATTCTCCAACCCAAAGTATTCTTCTTTTCTTAGTTTCAGAAGTACTGGCATCACAC
 GCAGGTACCTTGGCGTGTGTCCCTGTGGTACCCTGGCAGAGAAGAGACCAAGCTTGTTT
 CCCTGCTGGCCAAAGTCAGTAGGAGAGGATGCACAGTTTGCTATTTGCTTTAGAGACAGG
 GACTGTATAACAAGCCTAACATTGGTGCAAAGATTGCCTCTTGAAAAAAAAAAAAA

FIGURE 3 (1)

ATGGCCCAAGCCCTGCCCTGGCTCCTGCTGTGGATGGGCGCGGGAGTGCTGCCTGCCCAC
 M A Q A L P W L L L W M G A G V L P A H
 GGCACCCAGCACGGCATCCGGCTGCCCCTGCGCAGCGGCCTGGGGGGCGCCCCCTGGGG
 G T Q H G I R L P L R S G L G G A P L G
 CTGCGGCTGCCCCGGGAGACCGACGAAGAGCCCGAGGAGCCCGGCCGGAGGGGCAGCTTT
 L R L P R E T D E E P E E P G R R G S F
 GTGGAGATGGTGGACAACCTGAGGGGCAAGTCGGGGCAGGGCTACTACGTGGAGATGACC
 V E M V D N L R G K S G Q G Y Y V E M T
 GTGGGCAGCCCCCGCAGACGCTCAACATCCTGGTGGATACAGGCAGCAGTAACTTTGCA
 V G S P P Q T L N I L V D T G S S N F A
 GTGGGTGCTGCCCCCACCCCTTCCTGCATCGCTACTACCAGAGGCAGCTGTCCAGCACA
 V G A A P H P F L H R Y Y Q R Q L S S T
 TACCGGGACCTCCGGAAGGGTGTGTATGTGCCCTACACCCAGGGCAAGTGGGAAGGGGAG
 Y R D L R K G V Y V P Y T Q G K W E G E
 CTGGGCACCGACCTGGTAAGCATCCCCATGGCCCCAACGTCACTGTGCGTGCCAACATT
 L G T D L V S I P H G P N V T V R A N I
 GCTGCCATCACTGAATCAGACAAGTTCTTCATCAACGGCTCCAAGTGGGAAGGCATCCTG
 A A I T E S D K F F I N G S N W E G I L
 GGGCTGGCCTATGCTGAGATTGCCAGGCCTGACGACTCCCTGGAGCCTTTCTTTGACTCT
 G L A Y A E I A R P D D S L E P F F D S
 CTGGTAAAGCAGACCCACGTTCCCAACCTCTTCTCCCTGCAGCTTTGTGGTGCTGGCTTC
 L V K Q T H V P N L F S L Q L C G A G F
 CCCCTCAACCAGTCTGAAGTGCTGGCCTCTGTGCGAGGGAGCATGATCATTGGAGGTATC
 P L N Q S E V L A S V G G S M I I G G I
 GACCACTCGCTGTACACAGGCAGTCTCTGGTATACACCCATCCGGCGGGAGTGGTATTAT
 D H S L Y T G S L W Y T P I R R E W Y Y
 GAGGTCATCATTGTGCGGGTGGAGATCAATGGACAGGATCTGAAAATGGACTGCAAGGAG
 E V I I V R V E I N G Q D L K M D C K E
 TACAACTATGACAAGAGCATTGTGGACAGTGGCACCACCAACCTTCGTTTGCCCAAGAAA
 Y N Y D K S I V D S G T T N L R L P K K
 GTGTTTGAAGCTGCAGTCAAATCCATCAAGGCAGCCTCCTCCACGGAGAAGTTCCCTGAT
 V F E A A V K S I K A A S S T E K F P D

FIGURE 3 (2)

GGTTTCTGGCTAGGAGAGCAGCTGGTGTGCTGGCAAGCAGGCACCACCCCTTGGAACATT
G F W L G E Q L V C W Q A G T T P W N I

TTCCAGTCATCTCACTCTACCTAATGGGTGAGGTTACCAACCAGTCCTTCCGCATCACC
F P V I S L Y L M G E V T N Q S F R I T

ATCCTTCCGCAGCAATACCTGCGGCCAGTGGAAGATGTGGCCACGTCCCAAGACGACTGT
I L P Q Q Y L R P V E D V A T S Q D D C

TACAAGTTTGCCATCTCACAGTCATCCACGGGCACTGTTATGGGAGCTGTTATCATGGAG
Y K F A I S Q S S T G T V M G A V I M E

GGCTTCTACGTTGTCTTTGATCGGGCCCCGAAAACGAATTGGCTTTGCTGTCAGCGCTTGC
G F Y V V F D R A R K R I G F A V S A C

CATGTGCACGATGAGTTCAGGACGGCAGCGGTGGAAGGCCCTTTTGTACCTTGGACATG
H V H D E F R T A A V E G P F V T L D M

GAAGACTGTGGCTACAACATTCCACAGACAGATGAGTCAACCCTCATGACCATAGCCTAT
E D C G Y N I P Q T D E S T L M T I A Y

GTCATGGCTGCCATCTGCGCCCTCTTCATGCTGCCACTCTGCCTCATGGTGTGTCACTGG
V M A A I C A L F M L P L C L M V C Q W

CGCTGCCTCCGCTGCCTGCGCCAGCAGCATGATGACTTTGCTGATGACATCTCCCTGCTG
R C L R C L R Q Q H D D F A D D I S L L

AAGTGAGGAGGCCCATGGGCAGAAGATAGAGATTCCCCTGGACCACACCTCCGTGGTTCA
K

CTTTGGTCACAAGTAGGAGACACAGATGGCACCTGTGGCCAGAGCACCTCAGGACCCTCC
CCACCCACCAAATGCCTCTGCCTTGATGGAGAAGGAAAAGGCTGGCAAGGTGGGTTCAG
GGACTGTACCTGTAGGAAACAGAAAAGAGAAGAAAGCACTCTGCTGGCGGGAATACT
CTTGGTCACCTCAAATTTAAGTCGGGAAATTCTGCTGCTTGAAACTTCAGCCCTGAACCT
TTGTCCACCATTTCCTTTAAATTCTCCAACCCAAAGTATTCTTCTTTCTTAGTTTCAGAA
GTACTGGCATCACACGCAGGTTACCTTGGCGTGTGTCCCTGTGGTACCCTGGCAGAGAAG
AGACCAAGCTTGTTTCCCTGCTGGCCAAAGTCAGTAGGAGAGGATGCACAGTTTGCTATT
TGCTTTAGAGACAGGGACTGTATAAACAAGCCTAACATTGGTGCAAAGATTGCCTCTTGA
ATTAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 4

ATGGCCCCAGCGCTGCACTGGCTCCTGCTATGGGTGGGCTCGGGAATGCTGCCTGCCAG
 M A P A L H W L L L W V G S G M L P A Q
 GGAACCCATCTCGGCATCCGGCTGCCCCCTTCGCAGCGGCCTGGCAGGGCCACCCCTGGGC
 G T H L G I R L P L R S G L A G P P L G
 CTGAGGCTGCCCCGGGAGACTGACGAGGAATCGGAGGAGCCTGGCCGGAGAGGCAGCTTT
 L R L P R E T D E E S E E P G R R G S F
 GTGGAGATGGTGGACAACCTGAGGGGAAAGTCCGGCCAGGGCTACTATGTGGAGATGACC
 V E M V D N L R G K S G Q G Y Y V E M T
 GTAGGCAGCCCCCACAGACGCTCAACATCCTGGTGGACACGGGCAGTAGTAACCTTTGCA
 V G S P P Q T L N I L V D T G S S N F A
 GTGGGGGCTGCCCCACACCTTTCTGTCATCGCTACTACCAGAGGCAGCTGTCCAGCACA
 V G A A P H P F L H R Y Y Q R Q L S S T
 TATCGAGACCTCCGAAAGGGTGTGTATGTGCCCTACACCCAGGGCAAGTGGGAGGGGGAA
 Y R D L R K G V Y V P Y T Q G K W E G E
 CTGGGACCCGACCTGGTGAGCATCCCTCATGGCCCCAACGTCACTGTGCGTGCCAACATT
 L G T D L V S I P H G P N V T V R A N I
 GCTGCCATCACTGAATCGGACAAGTTCTTCATCAATGGTTCCAACCTGGGAGGGGCATCCTA
 A A I T E S D K F F I N G S N W E G I L
 GGGCTGGCCTATGCTGAGATTGCCAGGCCCCGACGACTCTTTGGAGCCCTTCTTTGACTCC
 G L A Y A E I A R P D D S L E P F F D S
 CTGGTGAAGCAGACCCACATTCCCAACATCTTTTCCCTGCAGCTCTGTGGCGCTGGCTTC
 L V K Q T H I P N I F S L Q L C G A G F
 CCCCTCAACCAGACCGAGGCACTGGCCTCGGTGGGAGGGAGCATGATCATTGGTGGTATC
 P L N Q T E A L A S V G G S M I I G G I
 GACCACTCGCTATACACGGGCAGTCTCTGGTACACACCCATCCGGCGGGAGTGGTATTAT
 D H S L Y T G S L W Y T P I R R E W Y Y
 GAAGTGATCATTGTACGTGTGGAAATCAATGGTCAAGATCTCAAGATGGACTGCAAGGAG
 E V I I V R V E I N G Q D L K M D C K E
 TACAACACGACAAGAGCATTGTGGACAGTGGGACCACCAACCTTCGCTTGCCCAAGAAA
 Y N Y D K S I V D S G T T N L R L P K K
 GTATTTGAAGCTGCCGTCAAGTCCATCAAGGCAGCCTCCTCGACGGAGAAGTTCCTCGGAT
 V F E A A V K S I K A A S S T E K F P D
 GGCTTTTGGCTAGGGGAGCAGCTGGTGTGCTGGCAAGCAGGCACGACCCCTTGGAACATT
 G F W L G E Q L V C W Q A G T T P W N I
 TTCCAGTCATTTCACTTTACCTCATGGGTGAAGTCACCAATCAGTCCCTTCGCGATCACC
 F P V I S L Y L M G E V T N Q S F R I T
 ATCCTTCCTCAGCAATACCTACGGCCGGTGGAGGACGTGGCCACGTCCCAAGACGACTGT
 I L P Q Q Y L R P V E D V A T S Q D D C
 TACAAGTTGCTGTCTCACAGTCATCCACGGGCAGTGTATGGGAGCCGTATCATGGAA
 Y K F A V S Q S S T G T V M G A V I M E
 GGTTTCTATGTCGTCTTCGATCGAGCCCGAAAGCGAATTGGCTTTGCTGTGACGCTTGC
 G F Y V V F D R A R K R I G F A V S A C
 CATGTGCACGATGAGTTCAGGACGGCGGCAGTGGAAAGTCCGTTTGTACGGCAGACATG
 H V H D E F R T A A V E G P F V T A D M
 GAAGACTGTGGCTACAACATTCCCCAGACAGATGAGTCAACACTTATGACCATAGCCTAT
 E D C G Y N I P Q T D E S T L M T I A Y
 GTCATGGCGGCCATCTGCGCCCTTTCATGTTGCCACTCTGCCTCATGGTATGTGAGTGG
 V M A A I C A L F M L P L C L M V C Q W
 CGCTGCCTGCGTTGCTGCGCCACCAGCAGATGACTTTGCTGATGACATCTCCCTGCTC
 R C L R C L R H Q H D D F A D D I S L L
 AAGTAAGGAGGCTCGTGGGCAGATGATGGAGACGCCCCCTGGACCACATCTGGGTGGTTCC
 K
 CTTTGGTCACATGAGTTGGAGCTATGGATGGTACCTGTGGCCAGAGCACCTCAGGACCCCT
 CACCAACCTGCCAATGCTTCTGGCGTGACAGAACAGAGAAATCAGGCAAGCTGGATTACA
 GGGCTTGACCTGTAGGACACAGGAGAGGGGAAGCAAGCAGCGTTCTGGTGGCAGGAATAT
 CCTTAGGCACCACAACTTGAGTTGGAAATTTTGTGCTGCTTGAAGCTTCAGCCCTGACCCT
 CTGCCCAGCATCCTTTAGAGTCTCCAACCTAAAGTATTCTTTATGTCCTTCCAGAAGTAC

TGGCGTCATACTCAGGCTACCCGGCATGTGTCCCTGTGGTACCCTGGCAGAGAAAGGGCC
AATCTCATTCCCTGCTGGCCAAAGTCAGCAGAAGAAGGTGAAGTTTGCCAGTTGCTTTAG
TGATAGGGACTGCAGACTCAAGCCTACACTGGTACAAAGACTGCGTCTTGAGATAAACAA
GAA

002250"4E89950

0906014-090200

10/20

FIGURE 6 (1)

ATGGCTAGCATGACTGGTGGACAGCAAATGGGTGCGGGATCCACCCAGCACGGCATCCGG
 M A S M T G G Q Q M G R G S T Q H G I R
 CTGCCCCTGCGCAGCGGCTGGGGGGCGCCCCCTGGGGCTGCGGCTGCCCCGGGAGACC
 L P L R S G L G G A P L G L R L P R E T
 GACGAAGAGCCCGAGGAGCCCGCGGAGGGGAGCTTTGTGGAGATGGTGGACAACCTG
 D E E P E E P G R R G S F V E M V D N L
 AGGGGCAAGTCGGGGCAGGGCTACTACGTGGAGATGACCGTGGGCAGCCCCCGCAGACG
 R G K S G Q G Y Y V E M T V G S P P Q T
 CTCAACATCCTGGTGGATACAGGCAGCAGTAACTTTGCAGTGGGTGCTGCCCCCACCCC
 L N I L V D T G S S N F A V G A A P H P
 TTCCTGCATCGCTACTACCAGAGGCAGCTGTCCAGCACATACCGGGACCTCCGGAAGGGC
 F L H R Y Y Q R Q L S S T Y R D L R K G
 GTGTATGTGCCCTACACCCAGGGCAAGTGGGAAGGGGAGCTGGGCACCGACCTGGTAAGC
 V Y V P Y T Q G K W E G E L G T D L V S
 ATCCCCCATGGCCCCAACGTCACTGTGCGTGCCAACATTGCTGCCATCACTGAATCAGAC
 I P H G P N V T V R A N I A A I T E S D
 AAGTTCTTCATCAACGGCTCCAAGTGGGAAGGCATCCTGGGGCTGGCCTATGCTGAGATT
 K F F I N G S N W E G I L G L A Y A E I
 GCCAGGCCTGACGACTCCCTGGAGCCTTTCTTTGACTCTCTGGTAAAGCAGACCCACGTT
 A R P D D S L E P F F D S L V K Q T H V
 CCCAACCTCTTCTCCCTGCAGCTTTGTGGTGCTGGCTTCCCCCTCAACCAGTCTGAAGTG
 P N L F S L Q L C G A G F P L N Q S E V
 CTGGCCTCTGTGCGGAGGGAGCATGATCATTGGAGGTATCGACCACTCGCTGTACACAGGC
 L A S V G G S M I I G G I D H S L Y T G
 AGTCTCTGGTATACACCCATCCGGCGGGAGTGGTATTATGAGGTCATCATTGTGCGGGTG
 S L W Y T P I R R E W Y Y E V I I V R V
 GAGATCAATGGACAGGATCTGAAAATGGACTGCAAGGAGTACAACATGACAAGAGCATT
 E I N G Q D L K M D C K E Y N Y D K S I
 GTGGACAGTGGCACCACCAACCTTCGTTTGCCCCAAGAAAGTGTGTTGAAGCTGCAGTCAAA
 V D S G T T N L R L P K K V F E A A V K
 TCCATCAAGGCAGCCTCCTCCACGGAGAAGTTCCTGATGGTTTCTGGCTAGGAGAGCAG
 S I K A A S S T E K F P D G F W L G E Q
 CTGGTGTGCTGGCAAGCAGGCACCACCCCTTGGAAACATTTTCCAGTCATCTCACTCTAC
 L V C W Q A G T T P W N I F P V I S L Y
 CTAATGGGTGAGGTTACCAACCAGTCCTTCCGCATCACCATCCTTCCGCAGCAATACCTG
 L M G E V T N Q S F R I T I L P Q Q Y L
 CGGCCAGTGGAAGATGTGGCCACGTCCCAAGACGACTGTTACAAGTTTGCCATCTCACAG

0966314-09200

FIGURE 6 (2)

R P V E D V A T S Q D D C Y K F A I S Q
TCATCCACGGGGCACTGTTATGGGAGCTGTTATCATGGAGGGCTTCTACGTTGTCTTTGAT
S S T G T V M G A V I M E G F Y V V F D
CGGGCCCGAAAACGAATTGGCTTTGCTGTCAGCGCTTGCCATGTGCACGATGAGTTCAGG
R A R K R I G F A V S A C H V H D E F R
ACGGCAGCGGTGGAAGGCCCTTTTGTACCTTGGACATGGAAGACTGTGGCTACAACATT
T A A V E G P F V T L D M E D C G Y N I
CCACAGACAGATGAGTCATGA
P Q T D E S *

002260"4E8960

FIGURE 7 (1)

ATGGCTAGCATGACTGGTGGACAGCAAATGGGTGCGGGATCGATGACTATCTCTGACTCT
 M A S M T G G Q Q M G R G S M T I S D S
 CCGCGTGAACAGGACGGATCCACCCAGCACGGCATCCGGCTGCCCCTGCGCAGCGGCCTG
 P R E Q D G S T Q H G I R L P L R S G L
 GGGGGCGCCCCCTGGGGCTGCGGGCTGCCCCGGGAGACCGACGAAGAGCCCGAGGAGCCC
 G G A P L G L R L P R E T D E E P E E P
 GGCCGGAGGGGCAGCTTTGTGGAGATGGTGGACAACCTGAGGGGCAAGTCGGGGCAGGGC
 G R R G S F V E M V D N L R G K S G Q G
 TACTACGTGGAGATGACCGTGGGCAGCCCCCGCAGACGCTCAACATCCTGGTGGATACA
 Y Y V E M T V G S P P Q T L N I L V D T
 GGCAGCAGTAACTTTGCAGTGGGTGCTGCCCCCACCCTTCCTGCATCGCTACTACCAG
 G S S N F A V G A A P H P F L H R Y Y Q
 AGGCAGCTGTCCAGCACATACCGGGACCTCCGGAAGGGCGTGTATGTGCCCTACACCCAG
 R Q L S S T Y R D L R K G V Y V P Y T Q
 GGCAAGTGGGAAGGGGAGCTGGGCACCGACCTGGTAAGCATCCCCATGGCCCCAACGTC
 G K W E G E L G T D L V S I P H G P N V
 ACTGTGCGTGCCAACATTGCTGCCATCACTGAATCAGACAAGTTCTTCATCAACGGCTCC
 T V R A N I A A I T E S D K F F I N G S
 AACTGGGAAGGCATCCTGGGGCTGGCCTATGCTGAGATTGCCAGGCCTGACGACTCCCTG
 N W E G I L G L A Y A E I A R P D D S L
 GAGCCTTTCTTTGACTCTCTGGTAAAGCAGACCCACGTTCCCAACCTCTTCTCCCTGCAG
 E P F F D S L V K Q T H V P N L F S L Q
 CTTTGTGGTGGCTGGCTTCCCCCTCAACCAGTCTGAAGTGGTGGCCTCTGTGCGAGGGAGC
 L C G A G F P L N Q S E V L A S V G G S
 ATGATCATTGGAGGTATCGACCACTCGCTGTACACAGGCAGTCTCTGGTATACACCCATC
 M I I G G I D H S L Y T G S L W Y T P I
 CGGCGGGAGTGGTATTATGAGGTCATCATTGTGCGGGTGGAGATCAATGGACAGGATCTG
 R R E W Y Y E V I I V R V E I N G Q D L
 AAAATGGACTGCAAGGAGTACAACATGACAAGAGCATTGTGGACAGTGGCACCACCAAC
 K M D C K E Y N Y D K S I V D S G T T N
 CTTTCGTTTGCCCAAGAAAGTGTGTTGAAGCTGCAGTCAAATCCATCAAGGCAGCCTCCTCC
 L R L P K K V F E A A V K S I K A A S S
 ACGGAGAAGTTCCCTGATGGTTTCTGGCTAGGAGAGCAGCTGGTGTGCTGGCAAGCAGGC
 T E K F P D G F W L G E Q L V C W Q A G
 ACCACCCCTTGGAACATTTTCCAGTCATCTCACTCTACCTAATGGGTGAGGTTACCAAC
 T T P W N I F P V I S L Y L M G E V T N

FIGURE 7 (2)

CAGTCCTTCCGCATCACCATCCTTCCGCAGCAATACCTGCGGCCAGTGGAAGATGTGGCC
Q S F R I T I L P Q Q Y L R P V E D V A
ACGTCCCAAGACGACTGTTACAAGTTTGCCATCTCACAGTCATCCACGGGCACTGTTATG
T S Q D D C Y K F A I S Q S S T G T V M
GGAGCTGTTATCATGGAGGGCTTCTACGTTGTCTTTGATCGGGCCCGAAAACGAATTGGC
G A V I M E G F Y V V F D R A R K R I G
TTTGCTGTCAGCGCTTGCCATGTGCACGATGAGTTCAGGACGGCAGCGGTGGAAGGCCCT
F A V S A C H V H D E F R T A A V E G P
TTTGTCACCTTGGACATGGAAGACTGTGGCTACAACATTCCACAGACAGATGAGTCATGA
F V T L D M E D C G Y N I P Q T D E S *

FIGURE 8 (1)

ATGACTCAGCATGGTATTTCGTCTGCCACTGCGTAGCGGTCTGGGTGGTGCTCCACTGGGT
 M T Q H G I R L P L R S G L G G A P L G -
 CTGCGTCTGCCCCGGGAGACCGACGAAGAGCCCGAGGAGCCCGGCCGGAGGGGCAGCTTT
 L R L P R E T D E E P E E P G R R G S F -
 GTGGAGATGGTGGACAACCTGAGGGGCAAGTCGGGGCAGGGCTACTACGTGGAGATGACC
 V E M V D N L R G K S G Q G Y Y V E M T -
 GTGGGCAGCCCCCGCAGACGCTCAACATCCTGGTGGATACAGGCAGCAGTAACTTTGCA
 V G S P P Q T L N I L V D T G S S N F A -
 GTGGGTGCTGCCCCCACCCTTCCTGCATCGCTACTACCAGAGGCAGCTGTCCAGCACA
 V G A A P H P F L H R Y Y Q R Q L S S T -
 TACCGGGACCTCCGGAAGGGCGTGTATGTGCCCTACACCCAGGGCAAGTGGGAAGGGGAG
 Y R D L R K G V Y V P Y T Q G K W E G E -
 CTGGGCACCGACCTGGTAAGCATCCCCATGGCCCCAACGTCACGTGTGCGTGCCAAACATT
 L G T D L V S I P H G P N V T V R A N I -
 GCTGCCATCACTGAATCAGACAAGTTCTTCATCAACGGCTCCAACCTGGGAAGGCATCCTG
 A A I T E S D K F F I N G S N W E G I L -
 GGGCTGGCCTATGCTGAGATTGCCAGGCCTGACGACTCCCTGGAGCCTTTCTTTGACTCT
 G L A Y A E I A R P D D S L E P F F D S
 CTGGTAAAGCAGACCCACGTTCCCAACCTCTTCTCCCTGCAGCTTTGTGGTGCTGGCTTC
 L V K Q T H V P N L F S L Q L C G A G F -
 CCCCCTCAACCAGTCTGAAGTGCTGGCCTCTGTGCGAGGGAGCATGATCATTGGAGGTATC
 P L N Q S E V L A S V G G S M I I G G I -
 GACCACTCGCTGTACACAGGCAGTCTCTGGTATACACCCATCCGGCGGGAGTGGTATTAT
 D H S L Y T G S L W Y T P I R R E W Y Y -
 GAGGTCATCATTGTGCGGGTGGAGATCAATGGACAGGATCTGAAAATGGACTGCAAGGAG
 E V I I V R V E I N G Q D L K M D C K E
 TACAACATATGACAAGAGCATTGTGGACAGTGGCACCACCAACCTTCGTTTGCCCCAAGAAA
 Y N Y D K S I V D S G T T N L R L P K K -
 GTGTTTGAAGCTGCAGTCAAATCCATCAAGGCAGCCTCCTCCACGGAGAAGTTCCCTGAT
 V F E A A V K S I K A A S S T E K F P D -
 GGTTCCTGGCTAGGAGAGCAGCTGGTGTGCTGGCAAGCAGGCACCACCCCTTGGAACATT
 G F W L G E Q L V C W Q A G T T P W N I -
 TTCCAGTCATCTCACTCTACCTAATGGGTGAGGTTACCAACCAGTCCTTTTCGCATCACC
 F P V I S L Y L M G E V T N Q S F R I T -
 ATCCTTCCGCAGCAATACCTGCGGCCAGTGGAAGATGTGGCCACGTCCCAAGACGACTGT
 I L P Q Q Y L R P V E D V A T S Q D D C -

FIGURE 8 (2)

TACAAGTTTGCCATCTCACAGTCATCCACGGGCACTGTTATGGGAGCTGTTATCATGGAG
Y K F A I S Q S S T G T V M G A V I M E -

GGCTTCTACGTTGTCTTTGATCGGGCCCGAAAACGAATTGGCTTTGCTGTCAGCGCTTGC
G F Y V V F D R A R K R I G F A V S A C -

CATTAG

H *

002260"4FE89960

FIGURE 9

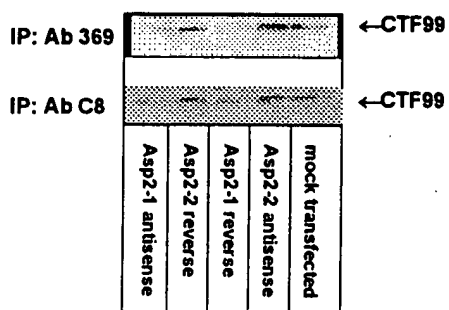


FIGURE 10

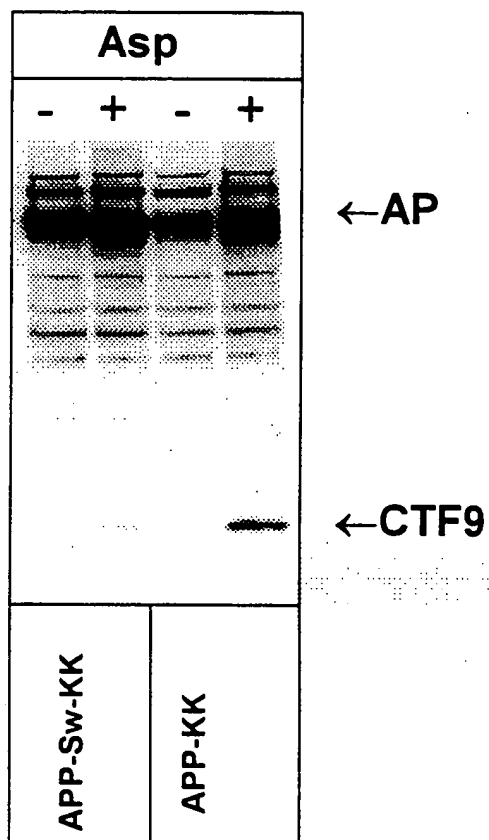


FIGURE 11

MAOALPWLLLWMGAGVLPAHGTQHGI~~R~~LPLRSGLGGA~~P~~LGLRLPRETDEE
PEEPGRRGSFVEMVDNLRGKSGQGYVEMTVGSPPQTLNILVDTGSSNFA
VGAAPHPFLHRYYQRQLSSTYRDLRKG~~V~~VPYTQGWEGELGTDLVSI~~P~~H
GPNVTVRANIAAITESDKFFINGSNWEGILGLAYAEIARPDDSLEPFFDS
LVKQTHVPNLFSLQLCGAGFPLNQSEVLASVGGSMIIGGIDHSLYTGSLW
YTPIRREWYYEVIIVRVEINGQDLKMDCKEYNYDKSIVDSGTTNLRLPKK
VFEEAVKSIKAASSTEKFPDGF~~W~~LGEQLVCWQAGTTPWNIFPVISLYLMG
EVTNQSFRITILPQYLRPVEDVATSQDDCYKFAISQSSTGTVMGAVIME
GFYVVFDRARKKRIGFAVSACHVHDEFRTAAVEGP~~F~~VTLDMEDCGYNIPQT
DES

FIGURE 12

MAOALPWLLLWMGAGVLPAGHTQHGIPLRLPLRSGLGAPLGLRLPRETDEE
PEEPGRRGSFVEMVDNLRGKSGQGYVEMTVGSPQTNLILVDTGSSNFA
VGAAPHPFLHRYYQRQLSSTYRDLRKGVPYPTQGKWEGLGTDLVSIPH
GPNVTVRANIAAITESDKFFINGSNWEGILGLAYAEIARPDDSLEPFFDS
LVKQTHVPNLFSLQLCGAGFPLNQSEVLASVGGSMIIGGIDHSLYTGSLW
YTPIRREWYYEVIIVRVEINGQDLKMDCKEYNYDKSIVDSGTTNLRPKK
VFEAAVKSIIKAASSTEKFPDGFVLGEQLVCWQAGTTPWNIFPVISLYLMG
EVTNQSFRTILPQQYLRPVEDVATSQDDCYKFAISQSSTGTVMGAVIME
GFYVVFDRARKRIGFAVSACHVHDEFRTAAVEGPFVTLDMEDCGYNIPQT
DESHHHHHH